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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein -
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                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                              DB DB
                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                             seq
   protein search, using
                                                                                                                                                                                                                                                                                                                                                             length:
                                                                                                                                                                                                                                                                                             SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria
3: sp_fung1:*
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Match
                                                                                                                                                                                                                                                                                                                                                                                                  671580 segs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
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564
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                                                                                                                                                                                          sp_unclassified:*
sp_rvirus:*
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  GenCore version 5.1.4_p5_4578 (c) 1993 - 2003 Compugen Ltd.
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Q9ZT62
Q9YWN6
Q8YWN6
Q942T6
Q9SBZ0
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Q9scm1
Q94a08
Q9m442
Q8rw08
Q9m4m7
Q9syj4
Q42099
                                                 Q93xk2
Q8rx87
Q40077
Q43408
                                                                              Q9fnd9
Q8vwn6
Q942t6
Q9sbz0
persea amer
arabidopsis
arabidopsis
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arabidopsis
cicer ariet
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hordeum vul
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parabidopsis
pisum sativ
coryza sativ
                      stachys aff
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
67	67	68		8	68.5	68.5			69		70.5	70.5	70.5	70.5	71	71	71	71	72	73	75	80	104.5	115	147.5	167	183	213
11.9	11.9	12.1	12.1	12.1	12.1	12.1	12.2	12.2	12.2	12.2	12.5	12.5	12.5	12.5	12.6	12.6	12.6	12.6	12.8	12.9	13.3	14.2	18.5	20.4	26.2	29.6	32.4	37.8
373	292	2026	329	219	216	183	2023	623	615	615	294	236	236	212	959	638	382	273	840	348	576	283	371	357	702	674	649	1170
υ	16	12	17	4	4	16	12	w	4	4	16	16	9					16				10	10	10	N	17	17	10
Q26960	Q9ABL5	Q9DJV1	Q8TWT1	Q9BVM4	Q9BT41	091177	091632	Q9P938	Q8TAP0	Q9NUX3	Q9S377	031962	064059	Q497.99	055716	804A60	Q970S3	Q9PN62	Q9LN46	Q94W95	Q9ZCM8	Q9FVM2	004607	Q39466	Q93CM6	Q96XG2	097094	Q9LFZ7
Q26960 trypanosoma	Q9ab15 caulobacter		Q8twtl methanopyru	Q9bvm4 homo sapien	7	Q911y7 pseudomonas	N			Q9nux3 homo sapien	Q9s377 mycobacter1	O31962 bacillus su	O64059 bacteriopha	Q49799 mycobacteri	055716 chilo iride	Q9vyu8 drosophila			σ	റ		Q9fvm2 arabidopsis		Q39466 cicer ariet	Q93cm6 bifidobacte		Q97u94 sulfolobus	Q9lfz7 arabidopsis

ALIGNMENTS

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RESULT 2
Q9FND9
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PKELL...

O92T62
O1-MAY-1999 (TrEMBLrel. 10, Created)
O1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
O1-MAY-2002 (TrEMBLrel. 20, Last annotation update)
O1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                   Ohsumi C., Nozaki J., Kida T.; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases EMBL; AF073744; AAD02832.1; -.
                                                                                                                                                                                                                                                                Cucumis sativus (Cucumber).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
 Q9FND9
                                                                                                                                                                                                                            TISSUE-LEAF;
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                         NCBI_TaxID=3659;
                                                   570
                                                                                          510
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                                                                                        TRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWCR 101
                                                                                                                                 101;
                                                                                                                                            Similarity
 PRELIMINARY;
                                                                                                                                   Conservative
                                                                                                                                         100.0%;
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                                                                                                                                          Score 564; DB 10;
Pred. No. 1.7e-54;
 PRT;
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783
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RESULT
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Q8VWN6;
01-MAR-2002
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                                                                                                        01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence up
01-MAR-2002 (TrEMBLrel. 20, Last annotation
Raffinose synthase (EC 2.4.1.82).
                                                                                                                                                                                                                                                                                                                                                                                                                   Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawa Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K. Bcker J., Theologis A., Davis R.W.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AB006702; BABIL595.1; -. EMBL; AY081645; AAM10207.1; -. EMBL; AY081645; AAM10207.1; -. EMBL; AY081645; AAM10207.1; -.
 SEQUENCE
                                     Pisum sativum (Garden pea).
Eukaryota; Viridiplantae; Strej
Spermatophyta; Magnoliophyta; eurosids I; Fabales; Fabaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kotani H., Nakamura Y., Sato S., Kaneko T., Asamızu E., Tabata S.; Trabata S.; Trabata S.; "Structural analysis of Arabidopsis thaliana chromosome Sequence features of the regions of 1,044,062 bp covered physically assigned Pl clones."; DNA Res. 4:291-300(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O9FND9;
01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                        NCBI_TaxID=3888;
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 FROM
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89.1%;
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16,
21,
                                                                Streptophyta;
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Last sequence up
Last annotation
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Pred. No. 1.5e-48;
                                                 eudicotyledons; core eu
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                                        Papilionoideae;
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                                       core eudicots;
vicieae; Pisum
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                                                                   Tracheophyta;
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Best I
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                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Galactinol-raffinose galactosyltransferase (EC 2.4.1.67).
Phaseolus angularis (Adzuki bean) (Vigna angularis).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Traci
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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01-DEC-2001
01-DEC-2001
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Q942T6;
                                                                                                                          Q9SBZ0;
                                                                                                                                                                                                                                                                                                                                                           Submitted (FEB-2001) to the EMBL/GenBank/DDBJ EMBL; AP003282; BAB64768.1; -. SEQUENCE 816 AA; 89588 MW; B316EDF3566C51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
        NCBI_TaxID=3914;
                                                                                                                                                                                                                                                                                                                                                                                               clone: P0583G08
                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Putative raffinose P0583G08.2.
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SEQUENCE 798 AA; 88717 MW; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JAN-2002) to the EMBL/GenBank/DDBJ EMBL; AJ426475; CAD20127.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular characterization of raffinose synthase sativum L.) seeds.";
                                                                                                                                                                                                                                                                                                                                                                                                       "Oryza sativa nipponbare(GA3) genomic DNA,
Clone:D0583C08 ":
                                                                                                                                                                                                                                                                                                                                                                                                                          Sasaki T., Matsumoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
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ilarity 82.2%;
Conservative 1
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Last annotation
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Pred.
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Pred. No. 1.
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                                                                                                                                         857
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.3e-45;
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                                              Tracheophyta;
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ID OBRX87;

AC Q8RX87;

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE AT5920250/F5024_140.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

C Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

Aurosids II; Brassicales; Brassicaceae; Arabidopsis.
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PHART J. 20:509-518(199).

EMBL; V19024; CAB64363.1; -.

ENDEL: V19024; CAB64363.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases EMBL; AJ311087; CAC38094.1; -. Glycosyltransferase; Transferase. SEQUENCE 853 AA; 95890 MW; CB10F18CBD37B38C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-CV. WUNDER VON KELVEDON; TISSUE-SEED Peterbauer T.;
"Molecular cloning of a cDNA encoding for s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; Spermatophyta; Magnoliophyta; eudicotyledons; vore eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoldeae; Vicleae; Pisum.
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Eukaryota; Viridiplantae; S
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95890 MW; CB10F18CBD37B38C CRC64;
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Pred. No. 9.
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Q43408;
Q43408;
01-NOV-1996
01-NOV-1996
01-DEC-2001
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Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou P.
Seki M., Southwick A., Tang C.C., Torlumi M., Wu H.C., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
Ecker J.R.:
                                                                                                                                                                                                                                                                                                                                                                                                   Spermatophyta; Magnoliophyta; Triticeae; Hordeum. NCBI_TaxID=4513;
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AY090237; AAL90901.1; -
SEQUENCE 844 AA; 94215 MW; 2AC8AB0EA43F8056 CRC64;
                                                                                                                                                                                                                                                                                imbibition in barley.";
Submitted (FEB-1992) to the EMBL/GenBank/DDBJ
EMBL; M77475; AAA32975.1;
SEQUENCE 757 AA; 82133 MW; EA9E7B771AABBCC
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Heck G.R., Dorsett C.,
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Eukaryota; Viridiplantae;
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yta; Liliopsida; Poales; Poaceae; Pooldea
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Pred. No. 2.9e-36;
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01-MAY-2000 (TrEMBLrel. 13, C
01-MAY-2000 (TrEMBLrel. 13, L
01-MAY-2000 (TrEMBLrel. 13, L
Imbibition protein homolog.
  Q94A08;
01-DEC-2001
01-DEC-2001
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Brassica oleracea (Cauliflower).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae: Rraceica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EU Arabidopsis sequencing project;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AL133248; CAB66109.1; -.
SEQUENCE 773 AA; 85143 MW; 0852F9E67952C8D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embry.
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Benes V., Rechmann S., Borkova D., Ansorge W., Mayer K.F.X., Quetier F., Salanoubat M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAY-1994) to the EMBL; X79330; CAA55893.1: -
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Fujikura Y., Karssen C.K.;
"Cauliflower cDNA encoding a putative imbibition protein.";
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     (TrEMBLrel.
                             (TrEMBLrel.
                                                                               PRELIMINARY;
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66.38;
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Last annotation updat
                             Created)
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Pred. No. 3
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. No. 3e-36;
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3.9e-36;
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edons; core eudicots; Rosidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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Best Local
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Q9M442;
Q1-QCT-2000 (TrEMBLrel. 15, Created)
Q1-QCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Q1-JUN-2001 (TremBLrel. 17)
                                                                                                                                                                                                                                                                                                                                                                      Cicer arietinum (Chickpea) (Garbanzo).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophy
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rc
eurosids I; Fabales; Fabaceae; Papilionoideae; Cicereae; Cicer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T. Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B. Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J. Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E., "Full Length cDNA of gene T8H10.120/AR7357520 (GI:6706423)."; "Full Length cDNA of gene T8H10.120/AR7357520 (GI:6706423)."; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AY050772; AAK92707.1; -
                                                                                                                                                                                                                  Submitted (JAN-2000) to the EMBL; AJ271668; CAB71135.1; NON_TER 1
                                                                                                                                                                                                                                                                                       STRAIN=CV.
Dopico B.,
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eeurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3827;
                                                                                                                                                                                                      SEQUENCE
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"A putative imbibition protein
150
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TRDCLFVDPARDRTSLLKIWNMNKCTGVVGVFNCQGAGWCK 190
                               TRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWCR 101
                                                                  PDWDMFHSLHPAAEYHAAARAIGGCPIYVSDKPGNHNFDLLKKLVLADGSVLRAQLPGRP
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                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                     CASTELLANA; TISSUE=ETIOLATED OSMOTIC
                                                                                                                                                                                                      386 AA;
                                                                                                                                   Conservative
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                                                                                                                                Score 392; DB 10;
Pred. No. 1.3e-35;
1; Mismatches 22;
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Pred.
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No. 3.9e-36;
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edons; core eudicots; Rosid
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                                                                                                                                                                   Length 386;
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RESULT
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Matches 65
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08RW08;
01-JUN-2002
01-JUN-2002
01-JUN-2002
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SEQUENCE 883 AA; 95227 MW; DD96FE666099DEFD CRC64;
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

STRAIN-CV. HASS: TISSUE-MESOCARP;
Zamorano J.P., Evans A.D., Dopico B., Lowe A.L., Wilson I.D.,
Merodio C., Grierson D.;
"Isolation and characterization of cDNAs for mRNAs regulated
cold storage of avocado (Persea americana Mill.) fruit.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ133148; CAB77245.1;
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SEQUENCE 779 AA; 85368 MW; C3A8B43160316785 CRC64;
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01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Persea americana (Avocado).
Eukaryota; Viridiplantae; Streptophyta;
Spermatophyta; Magnoliophyta; Laurales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Putative seed imbibition protein.
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"Molecular cloning of a cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=168825;
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                                                                                                                     PDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALP 60
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TRDSLFVDPARDGVSLLKIWNMNKCLGVVGVFNCQGAGWCK 582
                      TRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWCR 101
                                                                                           PDWDMEHSLHPAAEYHGAARAVGGCPIYVSDKPGHHNFELLKKLVLPDGSVLRARLPGRP
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(TrEMBLrel. 15, Last sequence up)
(TrEMBLrel. 19, Last annotation
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(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 21, Last annotation updaty)
ynthase (EC 2.4.1.67).
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Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core e eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
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Huang E.N., Nascimento L., de la Bastide M., Habermann K
Preston R.R., Spiegel L.A., See L.H., Shah R., Matero A.
O'Shaughnessy A., Rodriguez M., Shekher M., Swaby I., Sc
Parnell L.D., Dedhia N.N., McCombie W.R.;
"Arabidopsis thaliana BaC T7B11 from chromosome IV near
"Arabidopsis thaliana BaC T7B11 from chromosome IV near
submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EU Arabidopsis sequencing pr
Submitted (MAR-2000) to the
EMBL; AC007138; AAD22659.1;
EMBL; AL161493; CAB80690.1;
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completed: March ne : 59.6585 secs
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                                                                                                                                                    LPTRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGW 99
                                                                                                                LPTRDSLFKNPLFDKESILKIFNFNKFGGVIGTFNCQGAGW
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Query Match 71.1%; Score 401; DB 2; Length 765 Best Local Similarity 66.3%; Pred. No. 8.1e-35; Matches 67; Conservative 13; Mismatches 21; Indels

Length 765;

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1 PDWDMEQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALP 60

RESULT 2 945033 probable imbibition protein - wild cabbage C.Species: Brassica oleracea (wild cabbage) C.Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change C.Accession: \$45033 R.Fuljikura, Y. Karssen, C.K. submitted to the EMBL Data Library, May 1994 A.Description: Cauliflower cDNA encoding a putative imbibition A.Reference number: \$45033 A.Accession: \$	ALIGNMENTS RESULT 1 \$27762 Sip1 protein - barley C; Species: Hordeum vulgare (barley) C; Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Sep C; Accession: S27762 R; Heck, G.R.: Dorsett, C.; Ho, T.H. submitted to the EMBL Data Library, February 1992 A; Description: Cloning and characterization of a gene, Sip1, associate A; Reference number: S27762 A; Molecule type: DNA A; Residues: 1-757 <hec> A; Accession: S27762 A; Molecule type: DNA A; Residues: 1-757 <hec> A; Cross-references: EMBL:M77475; NID:g167099; PID:g167100 C; Genetics: A; Introns: 64/2; 151/1; 181/2; 197/3; 489/3; 557/2 Query Match Best Local Similarity 67.3%; Pred: No. 8e-35; Matches 68; Conservative 11; Mismatches 22; Indels 0; G Qy 1 </hec></hec>	30 64 11.3 486 2 T31294 hypother 31 64 11.3 674 2 G72204 hypother 32 63.5 11.3 402 1 MNXPC 1S1167, 36 63.5 11.3 418 2 H95197 1S1167, 36 63.5 11.3 418 2 H95208 IS1167, 36 63.5 11.3 418 2 H95208 IS1167, 37 63.5 11.3 418 2 H95208 IS1167, 38 63.5 11.3 418 2 H95208 IS1167, 39 63.5 11.3 418 2 H95208 IS1167, 39 63.5 11.3 418 2 H95208 IS1167, 39 63.5 11.3 429 2 C71075 Hypother 32 T31283 Hypother 63 11.2 108 2 T31283 hypother 63 11.2 252 2 F82640 hypother 63 11.2 252 2 F82640 hypother 63 11.2 884 2 S53396 telometrate 62.5 11.1 165 2 H71649 hypother
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C:Accession: C85025
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R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold R:anonymous, The Furopean Union Arabidopsis Genome Sequencing Consortium, The Cold R:anonymous, T69-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thallana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
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C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
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A; Introns: 64/2; 146/1; 176/2; 192/3; 223/2; 259/2; 300/2; 484/3; 507/2;
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A; Residues: 1-773 <BEN>
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A; Accession: T46188
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C;Accession: T46188
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N;Alternate names: protein T8H10.120
C;Species: Arabidopsis thaliana (mouse-ear cress)
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A; Residues: 1-807 <STO>
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                                                                                                                                                                                                                                                                                                 A;Gene: AT4g01970
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                                                                                                                                                                                                65.8%; Score 371; DB 2; Length 807 67.3%; Pred. No. 1.4e-31; tive 13; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70.9%; Score 400; DB 2; Length 773; 66.3%; Pred. No. 1e-34; tive 14; Mismatches 20; Indels
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C;Accession: C96599
C;Accession: C96599
C;Accession: C96599
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.
ansen, N.F.; Highes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin,
C.A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R
C.A.; Li, J.H.; Lin, X.; Lin, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: C95599
A;Status: preliminary
A: Laria trans- NNA
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R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awa: Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein SS03127 [imported] - Sulfolobus solfataricus C:Species: Sulfolobus solfataricus C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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A; Residues: 1-1170 <STO>
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A; Residues: 1-649 < KUR>
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Gene: SSO3127
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                                           YALPTROCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGG
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PALITEDLLFKDPLRE-RVLLKLKGKVKGYNAIAFFNLNSG
                                                                                                  PDYDMFMSYDPYAKVHLVARVFSGGPIYITD --- RHPERTNIELLRMAVLPNGEVIRVDE 511
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41.6%;
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Pred. No. 1.9e-14;
2; Mismatches 15
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.5e-11;
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goc, H.P.; Red
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Redder
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A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus A;Reference number: A70300; MUID:98196666; PMID:9537320 A;Accession: F70392
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R;Scheet, P.; Maggi, L.
submitted to the EMBL Data Library, June 1997
submitted to the sequence of A. thaliana IG
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 24-Mar-1999
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C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
C;Accession: T09530
                                           A; Molecule type: DNA
A; Residues: 1-165 <AQF>
                                                                                                                                                                                                                         hypothetical protein aq_1075 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: F70392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, February 1996 A; Reference number: Z16718 \,
                                                                               A: Status: preliminary; nucleic acid sequence not shown; translation
                                                                                                                                                               Nature 392, 353-358, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-371 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Description: The sequence A; Reference number: Z14407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: T01717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-357 <CER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Cervantes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable seed inhibition protein - chickpea (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:AF007269; NID:g2191126; PID:g2191156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: germinating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: EMBL: X95875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: T01717
                         Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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A_IG002N01.5
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                                                                                                                                                                                                                                                                                                                                                                                                         PDWDMFQST----HPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSIL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDWDMFHSLHPAAEYHAAARAIGGCQFMSVISQATTILIFLRSLVLADGS
                                                                                                                                                                                                    G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
25; Conserv
    source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                    GB:AE000721; NID:g2983544; PIDN:AAC07132.1; PID:g2983558; GB:AE00065
  strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cultivar Columbi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 115; DB
; Pred. No. 0.000
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 104.5;
Pred. No. 0.00
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       -QVIISDKPGQHDFNLLRKLVLQDGSIL 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240/1;
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Query Match
Best Local Similarity
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R; Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, I.C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, Nature 403, 665-668, 2000
A; Title: The genome sequence of the food-borne pathogen Campylobacter jejuni A; Reference number: A81250; MUID:20150912; PMID:10688204
A; Accession: E81330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: The genome sequence of Rickettsia A;Reference number: A71630; MUID:99039499; A;Accession: B71676
A; Gene:
                                        A; Cross-references: GB:AL139077; A; Experimental source: serotype
                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-273 <PAR>
                                                                                                                                                                                                                                                                                         C; Accession: E81330
                                                                                                                                                                                                                                                                                                          C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Keywords: ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AJ235272; GB:AJ235269; NID:g3861033; PIDN:CAA15132.1; A;Experimental source: strain Madrid E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-576 < AND>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark Nature 396, 133-140, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Nov-2000 C;Accession: B71676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Species:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable ABC transporter msbA2 - Rickettsia prowazekli
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                                                                                                                                                                                                                                                                                                                                                         probable periplasmic protein Cj1235 [imported] - Campylobacter jejuni (strain
                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;354-548/Domain: ATP-binding cassette homology <ABC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: msbA2; RP696
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                     Genetics
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       282 YYAIIAGVSSGGI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 FHAASRAISGGPIYVSDSVGKHNFDLLKKLVLP------DGSILRSEYYALPTR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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les 28; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DAISIEFKNVDFTYNSRPNLKVINNMSLKINSNKFVGIVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rickettsia prowazekii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rickettsia prowazekii probable ABC transporter msbA2;
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                                        GB:AL111168; NID:g69684444; PIDN:CAB73489.1; O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 75;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 76.5; DB Pred. No. 0.79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     331
                                                                                                                                                                                                                                               D.; Chil
d, S.; Bar
                                                             PID: g696
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12.6%; 26.0%;

Score Pred.

71; No.

5.6;

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Length

273;

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RESULT
T12810
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C;Date: 19-Mar-1997 #sequence_revision 25-Apr-199

C;Accession: S72873

R;Smith, D.R.; Robison, K.

submitted to the EMBL Data Library, November 1993

A;Description: Mycobacterium leprae cosmid B2126.

A;Reference number: S72585
                                                                                                                                                              В
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A; Residues: 1-212 <SMI>
A; Cross-references: EMB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Chilo iridescent virus
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999
C;Accession: T03053
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A; Status: preliminary
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Virus Genes 15, 235-245, 1997
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                                                                                  В
                                                                                                                                                                                                                                                                                                                             A; Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein B2126_F2_70 - Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: EMBL: AF003534; NID: g2738385; PIDN: AAB94427.1; PID: g2738400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-959 <BAH>
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                                                                                                                                                                                                                                                                                                                                                   ;Genetics:
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                                                                                  174 --- GWC 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     293 GKIIKVWNGNEFSSV 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19
                                                                                                                      95 QGGGWC 100
                                                                                                                                                                                                     41 LKKLVLPDGSILRSEYYALPTRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFN-----C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 -TMLKIWNLNKFTGV 88
                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SRAISGGP-IYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALPTRDCLFED---PLHNGE 74
                                                                                                                                                            LRLIYLADSQLLD---YA-PDRDEL----LRFGKTLMAIWRTIQFSGETGDFRPNPSRLC 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRMKTGEPYICFIDTCNKHMYDFQKKKGL---TIKQSNLCVAPETMILTEDGQFPIKDLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAFHAAS--RAISGGPIYVSDS----VGKHNFDLLKKLVLPDGSILRSEYYALPTRDCLF 66
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                                                                                                                                                                                                                                                                  12.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17;
                                                                                                                                                                                                                                                                  Score 70.5; DB 2; Pred. No. 4.7;
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Nature 409, 1007-1011, 2001
Nature 409, 1007-1011, 2001
A; Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.;
A; Title: Massive gene decay in the leprosy bacillus.
A; Title: Massive gene decay in the leprosy bacillus.
A: Peference number: A86909; MUID:21128732; PMID:11234002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997

A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galiech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosonó, S.; Hullo, M. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seakeuchi, M.; Tamakoshi, A.; Tananka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A; Reference number: A69580; MUID:98044033; PMID:9384377

A; Accession: F69912

A; Status: Outhors of the Gram of the Complete genome sequence of the Gram - Postitive bacterium Bacillus subtili A; Reference number: A69580; MUID:98044033; PMID:9384377
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C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 15-Oct-1999
C;Actes: T12810; F69912
C; Genetics:
                                                                                                                                                                          A; Reference number: A86909; A; Accession: B87073
                                                                                                                                                                                                                                                                                                                                                                                               R; Cole, S.T.; Eiglmeier, K.; Parkhill, R.; Davies, R.M.; Devlin, K.; Duthoy, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: B87073
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R;Kunst, F.; Ogasawara, N.; Moszer, I.; Alberlini, A.M.; Alloni, G.; Azevedo, V.; Ber
C.; Bron, S.; Broulllet, S.; Bruschi, C. V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
                                                                A; Molecule type: DNA
A; Residues: 1-294 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conserved hypothetical protein ML1312 [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein yomV - Bacillus subtilis phage SPBc2
C;Species: Bacillus subtilis phage SPBc2
                                  A;Cross-references:
                                                                                                                                            A; Status: preliminary
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A;Experimental source: strain 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -DMHCITEDKVVDNDELQEFHDISKSLKQQDSQSDLKDIVSCVAAFN 162
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                                  GB:AL450380;
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21.5%;
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                              NID:g13093231;
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Pred. No. 5
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S.; Feltwell, T.;
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                                  PIDN:CAC31693.1; GSPDB:GN00147
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Fraser, A
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  SwissProt_40:*
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  GenCore version 5.1.4_p5_4578 (c) 1993 - 2003 Compugen Ltd.
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VN34_ROTPC
BBS2_RAT
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SYE_AERPE
FLA3_PYRKO
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TERT_YEAST
NIA_NEUCR
Y872_RICPR
API2_SOLTU
YC56_PORPU
NPP_BPP2
RNP1_YEAST
MOTY_VIBPA
CELF_VZVD
PAP1_XENLA
IF2P_PYRHO
RHOD_HUMAN
SOML_GADMO
DAPA_RICCN
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VAA1_HUMAN
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3 saccharomyc
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9 pyrococcus
8 treponema p
5 saccharomyc
6 mus musculu
9 jiardia ima
9 haemophilus
6 porcine rot
9 rattus norv
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buchnera ap
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homo sapien
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vibrio para
varicella-z
xenopus lae
 homo sapien
gadus morhu
rickettsia
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bacteriopha
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RESULT 2
SYE_ARREE
ID SYE_ARREE
AC 09Y9H1:
DT 30-MAY-2000 0
DT 16-OCT-2001

STANDARD;

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(Rel. 39, Created)
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(Rel. 40, Last annotation update)

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SEYYALPTRDCLFEDPLHNGETMLKIWNLNKFTGV 88

IEFY----RYLRYKSPKYGPSFRSEYW----FIGV 164

Query Match Best Local S Matches 28

Similarity

13.6%;

Conservative

12;

Score 76.5; DI Pred. No. 0.22 12; Mismatches

DB . 22;

Length 165; Indels

36; 1:

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Gaps

9

1 PDWDMFQSTHPCAAFHAASRAISGGPIYVSDS--VGKHNFDLLKKLV---LPDGSIL--R 53

PKWIMFAARLPNGKLHPK----SGGKYYREDAVIVGEGNYELENPFISFKYSDGRILNFR 137

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                                                                                                                                                                                       RESULT
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A Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosi
A Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
A Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
A Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
A Yamazaki J., Kushida N., Sako Y., Kikuchi H.;
T. Nomura N., Sako Y., Kikuchi H.;
T. Complete genome sequence of an aerobic hyper-thermophilic
T. Crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
C -!- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
C diphosphate + L-glutamyl-tRNA(Glu).
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HSSP; P00962; 1GTR
                           Pyrococcus kodakaraensis
Archaea; Euryarchaeota;
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InterPro; IPR001412; tRNA-synt_1.
pfam; pF00749; tRNA-synt_1c; 1.
pRINTS; PR00987; TRNASYNTHGLU.
                                                                             Flagellin
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16-OCT-2001
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PROSITE; PS00178; AA_TRNA_LIGASE_I;
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                                                                                                                        16-OCT-2001
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                              Thermococci;
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5; Mismatches
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Best Local :
                                            "COMPACT SPIT OF THE MRAZ FAMILY SCIENCE 281:375-388(1998).

SCIENCE 281:375-388(1998).

THE MRAZ FAMILY SPIT OF THE MRAZ FAMILY THE IS
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O83398;
                                                                                                                                            Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J. Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garlan Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.
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Nagahisa K., Ezaki S., Fujiwara S., Imanaka T., Takagi M.;
Nagahisa K. Ezaki S., Fujiwara S., Imanaka T., Takagi M.;
Sequence and transcriptional studies of five clustered flagellin
genes from hyperthermophilic archaeon Pyrococcus kodakaraensis KO
FEMS Microbiol. Lett. 178:183-190(1999)
             the
                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - {\sf EMBL}
                                                                                                                                                                                                                                                                                                               Treponema pallidum.
Bacteria; Spirochaetales;
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                                                                                                                    "Complete genome sequence of Treponema pallidum,
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            European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
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                                                                                                                                                    А́Н.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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RESULT 5
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                                    Query Match
Best Local S
Matches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 29
                                                                                                Pfam; PF00440; HSF_DNA_bind; 1.
ProDom; PD001788; HSF_DNA_bind; 1.
SMART; SM00415; HSF; 1.
SMART; SM00415; HSF; DOMAIN; FALSE_NEG.
HYPOthetical protein; Nuclear protein; DNA_BIND 12 116 BY SIMILARITY
DNA_BIND 12 116 BY STOCKHITZEGO
                                                                                                                                                                                 EMBL: Z49646; CAA89680.1; -.
HSSP; P22121; 2HTS.
TRANSFAC; T03449; -.
SGD; S0003908; YJR147W.
InterPro; IPR000232; HSF_DNA_bind.
InterPro; IPR003341; HSF_ETS.
                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                           Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases -- SUBCELLULAR LOCATION: Nuclear (Potential). -- SIMILARITY: BELONGS TO THE HSF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 41.2 kDa protein in RPS4A-BAT2 i
YJR147W OR J2204.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YJ9L_YEAST
P47175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF02381; UPF0040; 2. TIGRFAMS; TIGR00242; TIGR00242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE001217; AAC65367.1; -. TIGR; TP0383; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed
                                                                                                                                                                                                                                                                              or send an
                                                                                                                                                                                                                                                                               entitles requires a license agreement (s or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 EKDCLILGLSH----CLEIWDRARY 126
            15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WDMFQSTHPCAA--FHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALP 60
            FHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WDRFSSQISARASLFHAPSRAVLRRLIAPAQEV --- ELDRAWRLFIPPS--LR-EYAAL- 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29;
                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR003444; UPF0040.
                                                                                          358 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17095 MW;
                                                                                          41192 MW;
                                                   11.48; 26.48;
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34.1%;
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                                                   Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 66.5;
Pred. No. 2
                                                              Score 64.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                          E2964157FC952D42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9CA9465EC5AAE850 CRC64;
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                                     Mismatches
                                                   NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        358
                                                                                                                                                                                                                                                                                           (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (See http://www.isb-sib.ch/announce/
                                                                                                                  DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces
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            ---- LRSEYYAL----
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4.
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                                     24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomycetes;
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                                                              Length 358;
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                                       Indels
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                                       33;
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             PTRD 63
                                     Gaps
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Q60696;
 CARBOHYD
CARBOHYD
CARBOHYD
VARIANT
                                          DOMAIN
REPEAT
                                                                                                                                                   TRANSMEM DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 23:154-158(1995).

-!- FUNCTION: COULD BE A MELANOGENIC ENZYME.
-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-!- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN MELANOCYTES.
-!- DISEASE: DEFECTS IN SILV ARE THE CAUSE OF THE SILVER COAT CO WHICH SEEMS TO BE DUE TO PREMATURE DEATH OF PIGMENT CELLS DU
                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                    This
                                                                                                                                                                                                                                               InterPro; IPR000601; PKD_domain.
Pfam; PF00801; PKD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Last annotation update)
Melanocyte protein Pmel 17 precursor (Silver locus
SILV OR PMEL17 OR D10H12S53E OR SI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel.
01-NOV-1997 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                   CHAIN
                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                        Disease mutation
                                                                                                                                                                                                                                       SMART; SM00089; PKD;
                                                                                                                                                                                                                                                                                 EMBL; U14133; AAA69538.1;
                                                                                                                                                                                                                                                                                                                                                           between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             putative cytoplasmic domain of Pmel Nucleic Acids Res. 23:154-158(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bennett D., Pickard R.T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kwon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/6; TISSUE=Skin; MEDLINE=95175358; PubMed=7870580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                   Transmembrane;
                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                       MGD; MGI:98301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse silver mutation is caused by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186
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                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE PMEL-17/MMB FAMILY.
SIMILARITY: CONTAINS 1 PKD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                              THE HAIR CYCLE
                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B.S., Halaban R., Ponnazhagan S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELSETP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLFEDPLHNGETMLKIWNLNKFTGVIGAFNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FHA------YQTANFLQENFEAIKKVVCPDSCLQHQQRQPKRPKRYSLLLLIPNAS 235
                                                                                                                                                                                                                             PS50093; PKD;
  563
584
315
315
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328
341
341
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367
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380
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1106
1111
                                                                                                                                                                                                                 Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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35, Last seq
  ----LMRFAGVFEFMNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence
 N-LINKED
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                                                                                                                              PKD.
7 X 13
                                                                                                                                                                                                                  Signal; Melanin biosynthesis;
                                                                                                                                                   CYTOPLASMIC
                                                                                                                                                             EXTRACELLULAR POTENTIAL.
                                                                                                                                                                                   MELANOCYTE PROTEIN PMEL
a single base insertion 17.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     626
                                                                                                                                                                                                                                                                                                               (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kim K.,
                                                                                                                                                                                                                                                                                                                                   There are no restrictions ong as its content is in
                                                                                                                              APPROXIMATE TANDEM
                                                                                                                                                  (POTENTIAL).
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           (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                          a collaboration -
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RESULT 7
                                            NOTE THE PRESENTATION OF T
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Matches
  Query Match
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Q03185;
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VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                            SEQUENCE
                                                                                                                                                                                                                   Pfam; PF03302; VSP; 1.
SMART; SM00181; EGF; 3
SMART; SM00261; FU; 5.
                                                                                                                                                                                                                                                                                                                                         EMBL; M95814; AAA02687.1;
PIR; A48579; A48579.
HSSP; P02468; 1KLO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Isolate AD-1;
MEDLINE=93241215; PunMed=8479449;
EY P.L., Khanna K., Manning P.A., Mayrhofer G.;
"A gene encoding a 69-kilodalton major surface
                                                                 CARBOHYD
                                                                                 CARBOHYD
                                                                                                                      TRANSMEM
                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      intestinalis trophozoites.";
Mol. Biochem. Parasitol. 58:247-258(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Giardia lamblia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Major surface
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15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                     DOMAIN
                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=5741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 TIINGSQVWGGQPVYPQEPDDACVFPDGGPCPSGPKPPKRSFVYVWKTWGKYWQVLG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN: CONTAINS 27 REPEATS OF A CXXC MOTIF. SIMILARITY: BELONGS TO THE GIARDIA VARIANT SURFACE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: TYPE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLASMA MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
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                                                                                                                                                                                                 Repeat; Transmembrane; Signal.
                                                                                                                                                                                                                                                                            IPR000561; EGF-like.
IPR002174; Furin-like.
IPR005127; Giardia_VSP
                                        634
663
591
630
667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diplomonadida;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 29, Created)
(Rel. 29, Last sequence up
(Rel. 36, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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373
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                                        N-LINKED (GLCNAC...) (P
N-LINKED (GLCNAC...) (P
1DD9572703232B8D CRC64;
                                                                                                                      MAJOR SURFACE TROPHOZOITE EXTRACELLULAR (POTENTIAL).
    Score
                                                                                                 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 64.5;
Pred. No. 21;
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(IN SILVER).
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Length
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                                                             (POTENTIAL)
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                                                                                                                                                            ANTIGEN 11
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    667;
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SILVER).
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GLPE_HAEIN
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Best Local
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Matches 18; Conser
                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F. Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M. McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Soott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Weitman J.F., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLPE_HAEIN STANDARD; PRT; 103 AA. PA4819; PA4819; O1-NOV-1995 (Rel. 32, Created) O1.NOV-1995 (Rel. 32, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Thiosulfate sulfurtransferase glpE (EC 2.8.1.1).
                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- FUNCTION: Catalyzes, although with low efficiency, the sulfur transfer reaction from thiosulfate to cyanide (By similarity).
-i- CATALYTIC ACTIVITY: Thiosulfate + cyanide = sulfite + thiocyanate.
-i- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-i- SIMILARITY: BELONGS TO THE GLPE FAMILY.
-i- SIMILARITY: CONTAINS 1 RHODANESE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rd."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=Rd / KW20 / ATCC 51907;
STRAINE=95350630; PubMed=7542800;
                                                                                                                                                                                                                                                    Pfam; PF00581; Rhodanese; 1.
                                                                                                                                                                                                                                                                                     HSSP; P09390;
TIGR; HI0679;
                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                          Transferase: Glycerol metabolism: Complete proteome ACT_SITE 63 63 BY SIMILARITY.
                                                                                                                                                                                                                                         SMART;
                                                                                                                                                                                                                                                                                                                      EMBL; U32750;
                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haemophilus.
NCBI_TaxID=727;
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                                                                                                                                                                                                                                                                        InterPro;
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                                DGSILRSEYYALPTRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWCR
                                                              WEMMQQGAILVDIRDNMRFAYSHPKGAFHLTNQ
                                                                                                                                                                                                                                         SM00450; RHOD;
                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                        IPR001763; Rhodanese-like
                                                                                                                                                                                         105 AA;
                                                                                                                            Conservative
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21.9%;
                                                                                             THPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLP
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                                                                                                                                          Score 64;
Pred. No.
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NVATFLVEQGYKNVFSMIGGFD---
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RESULT 9

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VN34_ROTPC

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Best Local S
Matches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-91361567; PubMed-1653496; Qlan Y.A., Jiang B.M., Saif L.J., Kang S.Y., Ojeh C.K., Green K.Y.; Qlan Y.A. Jiang B.M., Saif L.J., Kang S.Y., Ojeh C.K., Green K.Y.; Molecular analysis of the gene 6 from a porcine group C rotavirus that encodes the NS34 equivalent of group A rotaviruses."; Virology 184:752-757(1991).
STRAIN-Sprague-Dawley;
MEDLINE-21181710; PubMed-11285252;
Nishimura D.Y., Searby C.C., Carmi
                                                                                                                                                   15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Bardet-Biedl syndrome 2 protein homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Porcine rotavirus (group C / strain Cowden).
Viruses; dsRNA viruses; Reoviridae; Rotavirus.
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01-AUG-1992 (Rel. 23, 
15-JUL-1998 (Rel. 36,
                                                                                                                                                                                                                 Q99мн9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nonstructural protein; RNA-binding. DOMAIN 384 400 DRBM.
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Pfam; PF01665; Rota_NSP3; 1.
PROSITE; PS50137; DS_RBD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M69115; AAA47087.1; -.
                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A41040; MNXRPC.
InterPro; IPR0021159; DS_RBD.
InterPro; IPR002873; Rota_NSP3.
                                                                            NCBI_TaxID=10116;
                                                                                                                      Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                        258 NESPD--FD--VWNERSNLKIVSIND-CHAICVFKFENAWWC
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                                                                                                                                                                                                                                                                                                                                                                    SYNSTAAFVS---TIVGNPIKMYDESGKPLFDVGDYLNPKHIIDKMIENEIPIFKSDYRN 257
                                                                                                                                                                                                                                                                                                                                      LPTRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWC
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                                                                                          Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45125 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                           11.3%; Score 63.5;
27.5%; Pred. No. 16
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                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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There are no restrictions
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01-NOV-1997 (Rel. 35, Last sequence up
01-NOV-1997 (Rel. 35, Last annotation of the control of 
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                                                                                                                                           InterPro; IPR002557; Chitin_bind_PerA. Pfam; PF01607; CBM_14; 2. SMART; SM00494; ChtBD2; 1.
                                                                                                                                                                                                                                                                     modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. Th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polyhedrosis virus genome.";
Virology 229:381-399(1997).
-!- SIMILARITY: TO CORRESPONDING ORF IN ACMNPY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ahrens C.H., Russell Rohrmann G.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE-97271300; PubMed-9126251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Orgyła pseudotsugata multicapsid polyhedrosis virus (OpMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
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Hum. Mol. Genet. 10:865-874(2001).
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                                                                                                    SEQUENCE
                                                                                                                                                                                                                         EMBL; U75930; AAC59085.1; -
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"The sequence of the Orgyia |
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i., Sheffield V.C.;
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819 AA; 9
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L9; Mismatches
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Gorman S.M.
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30-MAY-2000
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                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extended the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
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CHARACTERIZATION.
MEDLINE-97274210; PubMed-9110970;
MEDLINE-97274210; PubMed-9110970;
MEDLINE-97274210; PubMed-9110970;
MEDLINE-97274210; PubMed-9110970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge Benes V. Bruckner M., Delius H., Dubois E., Dusterboft A., Entian K.D., Floeth M., Goffeau A., Hebling U., Heumann K., Entian K.D., Floeth M., Goffeau A., Hebling U., Heumann K., Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Kotter P., Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Mostl D., Mueller Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M. Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S., Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P., Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.; "The nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=S288c / AB972;
MEDLINE=97313267; PubMed=9169871;
                             InterPro; IPR000477; RVTse.
InterPro; IPR003545; Telomerase_RT
                                                                                    EMBL; U20618; AAB64520.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                          Science
                                                                                                                                                                                                                                                                                                                                                                                                                                            telomerase."
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reverse transcriptase motifs in the catalytic
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                                                                                                                                                                                                                                                                                                                ence 276:561-567(1997).
FUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL FOR THE REPLICATION OF CHROMOSOME TERMINI IN MOST EUKARYOTES. IT ELONGATES TELOMERES. IT IS A REVERSE TRANSCRIPTASE THAT ADDS SIMPLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY COPYING A TEMPLATE SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZYME.
SUBCELLULAR LOCATION: Nuclear:
                                                                                                                                                                                                                                                                                MISCELLANEOUS: DELETION CAUSES TELOMERE SHORTENING AND SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY
                                                                                                                                                                                                                                                                  TELOMERASE SUBFAMILY.
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(Rel. 39, Last sequence update)
(Rel. 40, Last annotation update)
reverse transcriptase (EC 2.7.7.-)
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RESULT 13
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01-MAY-1992
01-NOV-1995
                                                                                                                                                                       MEDLINE=>300000...
Okamoto P.M., Marzluf G.A.;
"Nitrate reductase of Neurospora crassa: the "Nitrate reductase of Neurospora crassa: the domain as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIA_NEUCR
P08619;
                                                                                                                                      site-directed mutagenesis.";
Mol. Gen. Genet. 240:221-230(1993).
-i- FUNCTION: NITRATE REDUCTASE IS A KEY ENZYME INVOLVED
                                                                                                                                                                                                                                                                                            Okamoto P.M., Garrett R.H., Marzluf G.A.; "Molecular characterization of conventional and new repeat-induced mutants of nit-3, the structural gene that encodes nitrate reductas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91287699; PubMed=1829499;
Okamoto P.M., Fu Y.-H., Marzluf G.A.;
"Nit-3, the structural gene of nitrate reductase in Neurospora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transferase; RNA-directed DNA polymerase; Telomere; Nuclear protein; DNA-binding.
SEQUENCE 884 AA; 102663 MW; 788334BB49592340 CRC64;
                                                                                                                                                                                                                                                                                                                                     STRAIN=74-OR23-1A;
MEDLINE=93241176; PubMed=8479443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         crassa: nucleotide sequence and regulation of mRNA synthesis
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STRAIN=74-OR23-1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neurospora
Eukaryota;
                                                                                                                                                                                                                          MEDLINE=93360901; PubMed=8355655;
                                                                                                                                                                                                                                         MUTAGENESIS
                                                                                                                                                                                                                                                                in Neurospora crassa.";
Mol. Gen. Genet. 238:81-90(1993).
                                                                                                                                                                                                                                                                                                                                                                   MUTANTS
                                                                                                                                                                                                                                                                                                                                                                                            in Neurospora crassa assimilatory nitrate reductase.";
EMBO J. 2:1909-1914(1983).
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Lе К.Н.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY PARTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76
        STEP OF NITRATE ASSIMILATION IN PLANTS, FUNGI AND BACTERIA.

CATALYTIC ACTIVITY: NADPH + nitrate = NADP(+) + nitrite + H(2)O.

COFACTOR: EACH SUBUNIT CONTAINS 1 EQUIVALENT OF FAD, HEME IRON,
AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME GROUP IS

CALLED CYTOCHROME B-557.

PATHMAY: NITRATE ASSIMILATORY PATHWAY.

SUBUNIT: HOMODIMER.

INDUCTION: ITS EXPRESSION IS HIGHLY REGULATED AND RESPONDS RAPIDLY
TO NITRATE INDUCTION AND TO NITROGEN REPRESSION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MLKIWNLNKFTGVIGAFN 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIYVSDSVGKHNFDLLKKL--VLPDGSIL----RSEYYALPTRDC--LFEDPL--HNGET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VRSQYFFNTNTGVLKLFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTQIADRIKEFKQRLLKKFNNVLPELYFMKFDVKSCYDSIPRMECMRILKDALKNENGFF 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 29.1
23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genet. 227:213-223(1991)
                                                                                                                                                                    amino acids in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Lederer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel.
(Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sordariaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 08, Created)
. 22, Last sequence upda
. 32, Last annotation up
e [NADPH] (EC 1.6.6.3) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ascomycota;
EUKARYOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.2%;
29.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neurospora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 63;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AROUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pezizomycotina;
 MOLYBDOPTERIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIS-652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 982 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                   examined
                                                                                                                                                                                              functional role
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                       IN THE
                                                                                                                                                                                                                                                                                               reductase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75
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                                                                RESULT 14
Y872_RICPR
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Best Local S
Matches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam: PF00173; heme_1; 1.—
Pfam: PF00174; oxidored_molyb; 1.
Pfam: PF00175; NAD_binding; 1.
Pfam: PF00175; NAD_binding; 1.
Pfam: PF00970; FAD_binding; 6; 1.
Pfam: PF00970; FAD_binding; 6; 1.
Pfam: PF009404; MO-CO_dimer; 1.
PFLNTS; PR00406; CYTBSRDTASE.
PRLNTS; PR00407; EUMOPTERIN.
PRINTS; PR00333; CYTOCHROMEB5.
PRINTS; PR001611; CYTC_B5; 1.
PROSITE; PS00151; CYTCCHROME_B5_1; 1.
PROSITE; PS00159; MOLYBDOTERIN_EUK; 1.
  30-MAY-2000
30-MAY-2000
16-OCT-2001
                                       Y872_RICPR
Q9ZC94;
                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
BINDING
BINDING
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a continuous the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                MUTAGEN
MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001199; Cyt_B5.
InterPro; IPR001334; Cyt_B5_reductase.
InterPro; IPR00572; Eut_Mb_oxred.
InterPro; IPR005066; Mo-co_dimer.
InterPro; IPR001433; Oxred_FAD/NAD(P).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X61303; CAA43600.1; -. PIR; S16292; S16292. PIR; S34796; S34796. PIR; S37298; S37298.
                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                          NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                   METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         iltrate assimilation
                                                                                                                 836
                                                                                                                                                                  782
                                                                                                                                                                                                                  736
                                                                                                                                       95
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                                                                                                                                                                                                                                         1 PDWDMFQ--STHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C-TERMINAL DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: CONTAINS 1 CYTOCHROME B5 FAMILY, HEME-BINDING DOMAIN. SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-TERMINAL DOMAIN
                                                                                                                 QGRGVC
                                                                                                                                       OCCCMC
                                                                                                                                                                SDGTLERGTLRVLVKIYYASPTED-----IKGGQMTQALDALALGKAVEFKGPVGKFVY 835
                                                                                                                                                                                      -----TMLKIWNLNKFTGVIGAFNC 94
                                                                                                                                                                                                                 PDTKIFHFALSHPAQSI------GLP-----VGQHLMMRLPDPAKPTESIIRAYTPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P00171;
                                                                                                                                                                                                                                                                               Similarity
                                                                                                                 841
                                                                                                                                                                                                                                                                                                                    982 AA;
(Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                       100
                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                240
295
499
621
675
718
952
6752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1F03
                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Flavoprotein;
                                                                                                                                                                                                                                                                                                                                 240
4995
652
675
982
961
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                                                                                                                                                                                                                                                                              11.28;
                                                                                                                                                                                                                                                                                                                    Μ¥.
                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                               Pred.
                                                                                                                                                                                                                                                                                                                                                                MOLYBDENUM-PTERIN (POTENTIAL).
MOLYBDENUM-PTERIN (POTENTIAL).
INTERCHAIN (POTENTIAL).
INTERCHAIN (POTENTIAL).
HEME LIGAND (BY SIMILARITY).
HEME LIGAND (BY SIMILARITY).
HEME LIGAND (BY SIMILARITY).
HEME LIGAND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                        Score
                                                                                                                                                                                                                                                                                                                                 H->A:
                                                                                                                                                                                                                                                                                                                                          NADP (BY SIMILARITY).
H->A: LITTLE LOSS OF ENZYME ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FAD;
                                                    PRT;
                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                    B7838C031B19687F CRC64;
                                                                                                                                                                                                                                                                               NO.
                                                                                                                                                                                                                                                                                          63;
                                                                                                                                                                                                                                                                                                                                LOSS OF ENZYME ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NADP; Heme;
                                                    165
                                                                                                                                                                                                                                                                              DB 1;
51;
                                                    Š
                                                                                                                                                                                                                                                                  3B;
                                                                                                                                                                                                                                                                                        Length 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molybdenum;
                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          restrictions
                                                                                                                                                                                                                                                                  46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                APIZ_SOLTU STANDARD; PRT; 220 AA. 043646; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Aspartic procease inhibitor 2 precursor (Cath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIL-Madrid E;
MEDLINE-99039499; PubMed-9823893;
Andersson S.G.E., Zomorodipour A., Andersson J.O.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M.,
Eriksson A.-S., Winkler H.H., Kurland C.G.;
                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-cv. AM 80.5793; TISSUE-Leaf;
MEDLINE-95036033; PubMed-7948907;
Herbers K., Prat S., Willmitzer L.;
                                                                                                                                                                                                                                                                Solanum tuberosum (Potato).

Eukaryota; Viridiplantae; Streptophyta; Embryospermatophyta; Magnoliophyta; eudicotyledons; Asteridae; euasterids I; Solanales; Solanaceae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mitochondria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                    Plant Mol.
                                                                                                                               Solanum tuberosum L.";
Plant Mol. Biol. 26:73-83(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ235273; CAA15296.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 396:133-140(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein RP872.
                                                                                                                                                                                                                                                    NCBI_TaxID=4113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=782;
                                                                                                                                                                                                                                                                                                                          (CathDinh)
                                                                                                                                                           Cloning and characterization of a cathepsin D inhibitor gene from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The genome sequence of Rickettsia prowazekii and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26
WOUNDING.
SIMILARITY:
FAMILY.
                                                       FUNCTION: INHIBITOR OF CATHEPSIN D (ASPARTIC PROTEASE). MAY ALSO INHIBIT TRYPSIN AND CHYMOTRYPSIN (SERINE PROTEASES). PROTECTS THE PLANT BY INHIBITING PROTEASES OF INVADING ORGANISMS. SUBCELLULAR LOCATION: Vacuolar (By similarity). TISSUE SPECIFICITY: TUBERS.
                                         INDUCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -NKFTGQENKIDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LNKFTGVIGAFNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIYVSDSVGKHNFDLLKKLVLPD--GSILR-SEYYALPTRDCLFEDPLHN-GETMLKIWN 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIYITDELQNPNNASVLVIISPTDIAKILQVKEYIKVFKRIIIITDLLENLKELIIKI-- 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                          (CathIhn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   al protein;
165 AA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prowazekii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                          TON
             BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152
                                          INDUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19411 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome.
9411 MW; 305290A3A14024C4 CRC64;
             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
             THE LEGUMINOUS KUNITZ-TYPE INHIBITOR
                                         BY ABSCISIC ACID, JASMONIC ACID AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 62.5; [Pred. No. 7.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                   Solanaceae;
                                                                                                                                                                                                                                                                                                                                       (Cathepsin
                                                                                                                                                                                                                                                                                            Embryophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                               core
                                                                                                                                                                                                                                                                   Solanum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                               eudicots;
                                                                                                                                                                                                                                                                                                                                          D inhibitor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Naeslund
                                                                                                                                                                                                                                                                                             Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of.
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in no way
commercial
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                                                                                                                                                                       Query Match
Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro: IPR002160; Kunitz_legume.
Pfam; PF00197; Kunitz_legume; 1.
PRINTS: PR00291; KUNITZINHBTR.
ProDom; PD000891; Kunitz_legume; 1.
SMART; SM00452; STI; 1.
SMART; SM00452; STI; 1.
PROSITE; PS00283; SOYBEAN_KUNITZ; 1.
ASPARTIC protease inhibitor; Serine p
Multigene family.
                                                                                                                                                                                                                                 DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                  SITE
                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
PROPEP
CHAIN
                                                                                                                                                                                                                                                                                                       ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                    ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X74985; CAA52919.1; -
                                                      100 FIPLSGGIFEDQLLNIQFNIATVKLCVSYTIWKVGNLNAY 139
                                                                     58 ALPTRDCLFEDPLHN-------GETMLKIWNLNKF 85
                                                                                                                                       10 HPCAAFHAAS--RAISGGPIYVS------DSVGKHNFDLLKKLVLPDGSILRSEYY 57
                                                                                                               49 NPNSSYRIISIGRGALGGDVYLGKSPNSDGPCPDGVFRYNSD-----VGPSGTFVR---- 99
                                                                                                                                                                                                                                 220 AA;
                                                                                                                                                                                                                                                80
174
51
                                                                                                                                                                                                                                                                                                       144
                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                    99
                                                                                                                                                                                                                                                                                                                                                                                                                                     SOYBEAN_KUNITZ; 1. inhibitor; Serine protease inhibitor; Signal;
                                                                                                                                                                                                                                 125 B
185 B
51 N
24199 MW;
                                                                                                                                                                                                                                                                                                                                                                23
32
220
31
                                                                                                                                                                                                                                                                                                          145
                                                                                                                                                                                                                                                                                                                                    100
                                                                                                                                                                                     11.1%; Score 62.5; DB 1; 25.0%; Pred. No. 11;
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                                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCMAC. . .) (POTENTIAL).
; 33D6E866EA0C5DD5 CRC64;
                                                                                                                                                                                                                                                                                       REACTIVE BOND (FOR TRYPSIN) (BY SIMILARITY).

REACTIVE BOND (FOR CHYMOTRYPSIN) (BY SIMILARITY).
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BY SIMILARITY.
                                                                                                                                                                       Mismatches
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Minimum DB
Maximum DB
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1: /cgn2_6/ptodata/1,

2: /cgn2_6/ptodata/1,

3: /cgn2_6/ptodata/1,

4: /cgn2_6/ptodata/1,

5: /cgn2_6/ptodata/1,

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564
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    Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/ABCTUS_COMB.pep:*
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US-08-854-050-55
US-09-430-323-55
US-08-804-227C-4
PCT-US93-04392-3
US-08-948-616-5
US-09-318-10-5
US-09-368-402-5
US-09-323-648-10
PCT-US93-04392-6
PCT-US93-04392-1
PCT-US93-04392-12
PCT-US93-04392-12
PCT-US93-04392-12
PCT-US93-04392-15
US-08-948-616-10
US-08-948-616-10
US-09-133-510-10
US-09-368-402-10
US-09-368-402-10
US-09-368-402-10
US-09-32-160-6
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US-09-153-586-23
US-08-851-843A-55
US-08-974-549A-222
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  Sequence
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  6, Appli
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11, Appl
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15, Appl
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US-09-255-829-29	US-09-255-829-22	US-09-255-829-24	US-08-370-476-114	US-08-481-985B-114	US-08-484-905-114	US-09-057-969-2	PCT-US95-05008-11	US-08-426-509A-11	US-09-251-645-6	PCT-US95-13830-2	US-09-296-219-2	US-08-766-982-2	US-08-666-082B-1	US-08-334-177-2	US-08-184-012C-8	US-09-296-219-11	US-08-944-483-55
Sequence 29, Appl	Sequence 22, Appl	Sequence 24, Appl	٠.	Sequence 114, App	Sequence 114, App	Sequence 2, Appli		Sequence 11, Appl	Sequence 6, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 8, Appli	Sequence 11, Appl	Sequence 55, Appl

ALIGNMENTS

RESULT 1

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                                                                                                                                                                                                                                 TELEFAX: (703)-413-220
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 784 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/08846234 Patent No. 6166292
                                                                                                                     Matches 101;
                                                                                                                                                     Query Match
                                                                                                                                         Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVEST. 22
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703).413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: OSUMI Chieko
APPLICANT: NOZAKI Jinshi
APPLICANT: KIDA Takao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: RAFFINOSE TITLE OF INVENTION: PRODUCING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: OBLON
STREET: 1755 S.
CITY: ARLINGTON
STATE: VIRGINIA
                                                    510
                  61
                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: UZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                                    PDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALP 60
                   TRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWCR 101
                                                    PDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALP
h 100.0%;
Similarity 100.0%;
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55 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                          protein
                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/846,234
                                                                                                                     0;
                                                                                                                     Score 564; DB 4;
Pred. No. 1.2e-64;
Mismatches 0;
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SEQ ID NO 23
LENGTH: 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 55,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 23, Application US/09153586A Patent No. 6270772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/153,586A CURRENT FILING DATE: 1998-09-15 EARLIER APPLICATION NUMBER: 60/064,552 EARLIER FILING DATE: 1997-09-16 EARLIER APPLICATION NUMBER: 60/064,555 EARLIER FILING DATE: 1997-10-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 48823
CURRENT APPLICATION N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Burrows et al.
TITLE OF INVENTION: Recombinant MHC molecules useful for manipulation
TITLE OF INVENTION: antigen-specific T-Cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                           APPLICANT: Andrews, William H.
TITLE OF INVENTION: NO. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
       PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/846,017
                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 -- IWRLEEF-AKFASFEAQG 148
FILING DATE:
                                                                    APPLICATION NUMBER: FILING DATE: 06-MA
                                                                                                                                                                                                                      ZIP:
                                                                                                                                                                                                                                     COUNTRY:
                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73
                                                                                                                         SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 LKIWNLNKFTGVIGAFNCQG 96
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                                                                                                                                                                                                                      94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5, Application US/08851843A 6093809
                                                                                                                                                                                                                                                                         San Francisco
                                                                                                                                                                                                                                   California
United States of America
                                                                                                                                                                                                                                                                                          E: Townsend and Townsend and Crew LLP Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                   Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lingner, Joachim
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                                                                  UMBER: US/08/851,843A
06-MAY-1997
25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thomas R
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26.2%;
                                                                                                                           Release #1.0, Version #1.30
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: APPLICANT:
                             FILING DATE: 01-OCT-PRIOR APPLICATION DATA:
                                                     PRIOR APPLICATION DATA:
PRIOR APPLICATION NIMBER: US 08/724,643
                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: APPLE, Randolph T.
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
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APPLICATION NUMBER: US 0
FILING DATE: 18-APR-1997
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                                                                                               FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                STREET: Two Embarcac
CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                  APPLICATION NUMBER:
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                 APPLICATION NUMBER:
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Morin, Gregg B.
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Chapman, Karen B.
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                                                                                                                                                                 PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                   Townsend and Townsend and Crew LLP Townsend and Townsend and Crew LLP Townsend and Crew LLP
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18-APR-1997
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29.5%;
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Pred. No.
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24;
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PRIOR APPLICATION DATA:

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                                                                                                                                                Sequence 55, Applicat Patent No. 6261836 GENERAL INFORMATION:
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                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
    APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: NO. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
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FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Protein LOCATION: 1.884 OTHER INFORMATION: OTHER INFORMATION:
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                                                                                                                                                                                                                                                              559 VRSQYFFNTNTGVLKLFN 576
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REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
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                                                                                                                                                                                                                                                                                         76 MLKIWNLNKFTGVIGAFN 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 884 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                        PTQIADRIKEFKQRLLKKFNNVLPELYFMKFDVKSCYDSIPRMECMRILKDALKNENGFF 558
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                                                                                                                                                                                 Application US/08854050
                                                                                      Nakamura, Toru
Chapman, Karen B.
                                                                                                                                     Cech, Thomas R
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                   Lingner, Joachim
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09-MAY-1997
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06-MAY-1997
ADDRESS:
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14-AUG-1997
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576÷0300
222:
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ESTp (L8543.12)"
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RESULT 6
US-09-430-323-55
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Best Local S
                                                                                                                       Sequence 55, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: not
TOPOLOGY: not rela
MOLECULE TYPE: pept
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
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LENGTH: 884 amino acid
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APPLICATION NUMBER: I
FILING DATE: 18-APR-
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APPLICATION NUMBER:
FILING DATE: 25-APR-
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                 559 VRSQYFFNTNTGVLKLFN 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/851,843 FILING DATE: 06-MAY-1997 CLASSIFICATION: 536
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REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 01
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SOFTWARE: PatentI
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CITY: San Francisco
                                                                                                                                                                                                                                                                                                  76 MLKIWNLNKFTGVIGAFN 93
                                                                                                                                                                                                                                                                                                                                                                   26 PIYVSDSVGKHNEDLLKKL--VLPDGSIL----RSEYYALPTRDC--LFEDPL--HNGET 75
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nes 23; Conserv
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   TITLE
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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E: peptide
 Andrews, INVENTION:
                                    Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
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                                                                                                     Lingner, Joachim
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William H.
No. 6309867el Telomerase
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                                                                                                                                                                                                                                                                                                                                                                                                    Score 63; DB Pred. No. 24; 15; Mismatches
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NUMBER OF SEQUENCES:

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MOLECULE TYPE: peptide;
SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-09-430-323-55
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Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                      Sequence 4, Application US/08804227C Patent No. 5876991
        APPLICANT: Kubstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTH;
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                     559 VRSQYFFNTNTGVLKLFN 576
STREET:
                                                                                                                                                                                                                                                                                                                                                                                                             76 MLKIWNLNKFTGVIGAFN 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 PIYVSDSVGKHNFDLLKKL--VLPDGSIL----RSEYYALPTRDC--LFEDPL--HNGET 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION TO THE PROPERTY APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/724,643 FILING DATE: 01-OCT-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 884 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTQIADRIKEFKQRLLKKFNNVLPELYFMKFDVKSCYDSIPRMECMRILKDALKNENGFF 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: not relevant TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/430,323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
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                                                                                                                                                                                           DeHoff, Bradley S.
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                                                                                    POLYKETIDE SYNTHASE GENES: 15
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29.5%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 884;
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US-08-804-227C-4
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Best Local Similarity
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NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: x-83
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                 ENOTH: 430 amino acid
                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/04392
TOPOLOGIE TYPE: CDN
                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/883,658
FILING DATE: MAY 15, 1992
                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2602 TTDP-AAFYAEFAERGYDYGPAFQGFTAGARHGEDVVAEVALPSGLVADARHHRL 2655
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Salazar, Felix H., Snyder, Roger C.
TITLE OF INVENTION: Enzymatic Process for Production
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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LENGTH: 3729 amino acids
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                                   STRANDEDNESS: doub
TOPOLOGY: circular
                                                                      TYPE:
                                                                                                                                                                                          CLASSIFICATION:
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SOFTWARE: ASCI(DOS)
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                                                                     AMINO ACID
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                                                                                     430 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Pred. No.
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                                                                  US-08-948-616-5
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Best Local S
Matches 25
Best Local
Matches 1
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                               Query Match
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INDIVIDUAL ISOLATE:
IMMEDIATE SOURCE:
CLONE: ZL511 1-2
                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 210 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: VESICLE TRANSPORT ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 530 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             308 L----MFEDHLTGG---AKKGHEDALNGPVGSFFAVG 337
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CITY: Palo Alto
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nes 25; Conserv
                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                  NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: U. FILING DATE: Herewith CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 LPTRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQG 96
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                                                                               LIBRARY: KERANOT02
CLONE: 2620104
                                                                                                                                  STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                     TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: UZIP: 94304
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STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HPDDPLATGKQVLAGGGNMNLVADGDFGGHGMFTTGENYLKVLKSLLANDGKLLSPEMVN 307
l Similarity 33.3
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25.5%; Pred. No. 18;
            10.6%;
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 10; Mismatches
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             Score 60; DB 2; Pred. No. 7.8;
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                               Length 210;
 Indels
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US-09-193-510-5
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                                   RESULT 11
US-09-368-402-5
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                                                                                                                                                          Query Match
Best Local Similarity 33.3
Conservative
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Sequence 5, Application US/09368402 Patent No. 6200790
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                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
LIBRARY: KERAN
CLONE: 2620104
                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: PF.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEPAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lal, Preeti
APPLICANT: Shah, Purti
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: VESICLE TRANSPORT ASSOCIATED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/193,510 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 3174 Por
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 VKGKPVHLHIWDTAGQDDYDRLRPLFYPDASVL
                                                                                                     60 VKGKPVHLHIWDTAGQDDYDRLRPLFYPDASVL 92
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                                                                                                                                   22 ISGGPI--YVSDSVGKHNFDLLKKLVLPDGSIL 52
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                                                                                                                                                                                                                                                                                                                                                         LENGTH:
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                                                                                                                                                                                                                                                                          KERANOT02
                                                                                                                                                                                                                                                                                                          SS: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diskette
                                                                                                                                                                                    10.6%; Score 60; DB 2; 33.3%; Pred. No. 7.8;
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                                                                                                                                                                                                       Length 210
                                                                                                                                                                      2
                                                                                                                                                                      Gaps
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GENERAL INFORMATION:

APPLICANT:

Hillman, Jennifer L. Lal, Preeti

1:

APPLICANT:

Corley, Neil C

Shah, Purvi

CORRESPONDENCE ADDRESS

ADDRESSEE:

Incyte Pharmaceuticals, Inc

TITLE OF INVENTION: VESICLE TRANSPORT ASSOCIATED PROTEINS NUMBER OF SEQUENCES: 11

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CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 179
LENGTH: 608
TYPE: PRT
ORGANISM: Pinus radiata
                                                              US-09-325-932A-179
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APPLICANT: Flinn, Barry
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                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                Best Local Similarity
                                                                                                                                                                                                           APPLICANT: Lasham, Annette TITLE OF INVENTION: Compositions affecting TITLE OF INVENTION: death and their use in FILE REFERENCE: 1022
                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
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STRANDEDNESS: si
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REGISTRATION NUMBER: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 650-845-4166
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Conservative
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              10.6%; Score 60;
21.4%; Pred. No.
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18;
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Mismatches
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                               DB 4;
                                                                                                                                                                                                                     programmed cell
the modification of forestry plant devel
48;
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Indels
26;
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Gaps
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CURRENT APPLICATION NUMBER: US/09/342,648
CURRENT FILING DATE: 1999-06-29
EARLIER APPLICATION NUMBER: 60/092,659
EARLIER FILING DATE: July 13, 1998
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Microsoft Office 97
SEQ ID NO 10
LENGTH: 890
TYPE: PRT
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US-09-342-648-10
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                                                                                                                COMPUTER READABLE FORM:
MEDJUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Freedman, Richard, Heefner, Donald L. APPLICANT: Phelphs, Trish, Roberts, Christopher R. APPLICANT: Salazar, Felix H., Snyder, Roger C. TITLE OF INVENTION: Enzymatic Process for Production NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Beck, Steven R., Cain, Robert O., APPLICANT: Freedman, Richard, Heefner, Donal
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STATE:
                                                           FILING DATE: 1 CLASSIFICATION:
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APPLICATION NUMBER: U
                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                19930514
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25.0%;
                       us/07/883,658
                                                                                                   PCT/US93/04392
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Pred. No.
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                                                                                                                                              Version
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                                                                                                                                                #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chan, Hardy W.
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SEQUENCE CHARACTERISTICS:

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PRIOR APPLICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/883,65

FILING DATE: MAY 15, 1992

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 430 amino acids

TYPE: AMINO ACID

STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: CDNA
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Zopfiella latipes
STRAIN: 780
INDIVIDUAL ISOLATE: ATCC #44575
IMMEDIATE SOURCE:
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ORGANISM: ZOP***
STRAIN: 780
INDIVIDUAL ISOLATE: /
IMMEDIATE SOURCE:
CLONE: Z1780-3A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 430 amino acids
TYPE: AMINO ACID
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: CDNA
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Beck, Steven R., Cain, Robert O., Chan, Hardy W. APPLICANT: Freedman, Richard, Heefner, Donald L. APPLICANT: Phelphs, Trish, Roberts, Christopher R. APPLICANT: Salazar, Felix H., Snyder, Roger C. TITLE OF INVENTION: Enzymatic Process for Production of NUMBER OF SEQUENCES: 15
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CITY:
STATE:
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                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 19930! CLASSIFICATION:
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AAW53570
AAW17417
AAW57888
AAY30144
ABB93664
AAY32075
AAW32075
AAW32074
AAW370142
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188.389 Million cell updates/sec
             Cucumber raffinose
Japanese artichoke
Amino acid sequenc
Herbicidally activ
Rapeseed raffinose
Mustard raffinose
Broad bean raffino
Amino acid sequenc
                                                                                                                                                                                                                                       Description
                                                                                                                                                                                            Cucumber raffinose
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111	64 11. 5 11.	67 11. 67 11.	221	69 12. 69 12.	12. 12.	14 . 12 .	15. 14.	36.	68.	68.	70. 69.	71.	75.	75.	79 79	87.	88.	88.	
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coccus elanoma	Herbicidally active Herbicidally actives Soluble fused MHC	proteir	Novel human diagno	Novel human secret Human protein sequ	iori c tamicu	sis la	110	Herbicidally activ	t raffino	ean raffin	Rice raffinose syn Corn raffinose syn	Corn raffinose syn	acid seq	H	Sugarbeet raffinos	Soybean raffinose	n raf	no acid seque	Soybean raffinose

ALIGNMENTS

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RESULT 1
AAW53570
PT PT PT PXX
                                                                                                                                        Claim 3; Pages 17-20; 26pp; Japanese
                         Raffinose synthase gene - useful for preparation of raffinose in transformed plant
                                                     WPI; 1998-264858/24.
N-PSDB; AAV22250.
                                                                                                                                                                JP10084973-A.
                                                                                                                                                                                  Cucumis sativus
                                                                                                                                                                                                    Cucumber; raffinose synthase; sucrose;
                                                                                                                                                                                                                     Cucumber raffinose synthase
                                                                                                                                                                                                                                        06-JUL-1998 (first entry)
                                                                                                                                                                                                                                                           AAW53570;
                                                                                                 26-JUL-1996;
26-APR-1996;
                                                                                                                             28-APR-1997;
                                                                                                                                               07-APR-1998
                                                                                                                                                                                                                                                                             AAW53570 standard; Protein; 784 AA
                                                                               (AJIN ) AJINOMOTO KK
                                                                                                 96JP-0198079
96JP-0107682
                                                                                                                             97JP-0111124.
                                                                                                                                                                                                     galactinol
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Soybean protein:

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RESULT 2
AAY11/417
ID AAY1
AC AAY1
AC AAY1
XX AAY1
AC Cucu
XX Raff
XX JP11
XX JP11
XX JP11
XX JP11
XX JP11
XX AY1
PF 24-C
XX WPI;
DR WPI;
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DR N-PE
XX WPI;
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Best Local (
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                                                                                                                                                                                                                                                                                                                                           The present invention describes a raffinose synthase, having an activity of forming raffinose from sucrose and galactinol. The raffinose synthase gene can be used for expression in a plant for the production of raffinose. The raffinose synthase can give raffinose from sucrose and galactinol efficiently. The present sequence represents raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is cucumber raffinose synthase, which forms raffinose from sucrose and galactinol, has an optimum pH of 6 to 8 and working temperature of 35 to 40 degrees C, has a molecular weight of 75 to 95 kDa by gel filtration or 90 to 100 kDa by PAGE and SDS-PAGE under reductive conditions and is inhibited by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-340516/29.
N-PSDB; AAX61238.
                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                            synthase from cucumber.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sucrose and galactinol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New raffinose synthase gene -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Raffinose synthase;
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                         61
                                                                                                                                                                                                Local Similarity
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                                                                                            1 PDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALP 60
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                                                                       PDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALP 569
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Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 25-27; 37pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  raffinose
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Amino acid sequence of a raffinose synthase protein.

26-OCT-1999

(first

entry)

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RESULT 3
AAW57888
IDW 57888
IDW 57888
IDW 57888
IDW 57888
IDW 5788
IDW 23-5
IDW 23-5
IDW 5788
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AAY30144
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid molecule encoding plant raffinose synthetase capable of producing raffinose, used as food additives with beneficial effects on gastrointestinal flora
AAY30144;
                                                           AAY30144 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 36-38; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oeda K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stachys sieboldii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gastrointestinal flora; Japanese artichoke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            food additives with beneficial effects on the gastrointestinal flora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SUMO ) SUMITOMO CHEM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP849359-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Raffinose synthetase; metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Japanese artichoke raffinose synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW57888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW57888 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                        401
                                                                                                                                                                                                                          461 TRDCLFEDPLHNGKTMLKIWNYNKFTGVVGTFNCQGGGWSR 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      570 TRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWCR 610
                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                   1 PDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALP 60
                                                                                                                                                                                                                                                           TRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWCR 101
                                                                                                                                                                                                                                                                                                                                                        PDWDMFQSTHPCAEFHAASRAISGGPIYVSDSVGKHNFELLRSLVLPDGSILRCDYYALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV40802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wantanabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96JP-0338673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97EP-0122417.
                                                              Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.3%;
89.1%;
                                                              587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           587 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 515; DB 19;
Pred. No. 4.4e-57;
                                                              AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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ABB93664
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                                                                                                                                                                                                                                                                                                                                                    В
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                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a raffinose synthase protein. The sequence is isolated from plant material. The protein forms raffinose by complexing alpha(1 to 6). D-galactosyl hydroxyl group of the 6C of D-glucose residue in sucrose molecules.
Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12; Page 30-31; 40pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JP11215984-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stachys sieboldii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Raffinose synthase;
                                                                                                                                                WO200210210-A2.
                                                                                                                                                                                                                          31-MAY-2002
                                                                                                                                                                                                                                            ABB93664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New raffinose synthase gene - is prepared from a plant material
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-511112/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-AUG-1999
                              WPI; 2002-269010/31.
                                                Tietjen K,
                                                                                                                             07-FEB-2002
                                                                                                                                                                 Arabidopsis thaliana
                                                                                                                                                                                    Herbicidal;
                                                                                                                                                                                                      Herbicidally active polypeptide
                                                                                                                                                                                                                                                               ABB93664 standard; Protein;
                                                                   (FARB ) BAYER AG
                                                                                      28-AUG-2001; 2001WO-EP09892
                                                                                                        28-AUG-2001; 2001WO-EP09892.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SUMO ) SUMITOMO CHEM CO LTD
                                                                                                                                                                                                                                                                                                               461 TRDCLFEDPLHNGKTMLKIWNYNKFTGVVGTFNCQGGGWSR 501
                                                                                                                                                                                                                                                                                                                                                    401
                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                 TRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWCR 101
                                                                                                                                                                                                                                                                                                                                                                                          90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ10003
                                                                                                                                                                                                                                                                                                                                                                                                                                587 AA;
                                                Weidler
                                                                                                                                                                                    plant; agriculture;
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97JP-0329006.
96JP-0338673.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97JP-0342899
                                                 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plant; sucrose; raffinose.
                                                                                                                                                                                                                                                                                                                                                                                                   91.3%;
89.1%;
                                                                                                                                                                                                                                                               783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Japanese.
                                                                                                                                                                                                                                                                                                                                                                                         S
                                                                                                                                                                                                                                                                                                                                                                                                 Score 515; DB 20;
Pred. No. 4.4e-57;
                                                                                                                                                                                                                                                                ξ
                                                                                                                                                                                     herbicide
                                                                                                                                                                                                       SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         6,
                                                                                                                                                                                                                                                                                                                                                                                                          Length 587;
                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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RESULT 6
AAY32075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                          30-APR-1998;
30-APR-1998;
04-DEC-1998;
10-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ABB90790-ABB94016) for herbicidally active compounds, comprising alighing and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                         /note=
Misc-difference 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to identifying target (ABB90790-ABB94016) for herbicidally active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from plant with nucleic acid or amino acid sequences from non-plant organisms - \,
N-PSDB; AAZ20210
                                                                                                                                                                                                            Misc-difference 148
                                                                                                                                                                                                                                               /note-
Misc-difference 143
                                                                                                                                                                                                                                                                    /note= "encoded by Misc-difference 132
                                                                                                                                                                                                                                                                                                Location/Qualifiers
Misc-difference 129
                                                                                                                                                                                                                                                                                                                                    Brassica napus
                                                                                                                                                                                                                                                                                                                                                                                                     17-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                          AAY32075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY32075 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful as herbicides.
          WPI; 1999-593144/51
                                                                                                                                  27-APR-1999;
                                                                                                                                                       03-NOV-1999
                                                                                                                                                                             EP953643-A2
                                                                                                                                                                                                                                                                                                                                                       Raffinose synthase; rapeseed; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                               Rapeseed raffinose
                               Watanabe E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      575
                                                    (SUMO ) SUMITOMO CHEM CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 PDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRDRLFEDPLHDGKTMLKIWNLNKYTGVIGAFNCQGGGWCR 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWCR 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PDWDMFQSTHPCAEFHAASRAISGGPIYISDCVGKHDFDLLKRLVLPNGSILRCEYYALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       783 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ID NO
                                Oeda K;
                                                                          98JP-0120550.
98JP-0120551.
98JP-0345590.
98JP-0351246.
                                                                                                                                99EP-0107430
                                                                                                                                                                                                   /note-
                                                                                                                                                                                                                                                                                                                                                                              synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.6%;
                                                                                                                                                                                                                                             "encoded
                                                                                                                                                                                                "encoded by CGR'
                                                                                                                                                                                                                        "encoded
                                                                                                                                                                                                                                                                 "encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        261pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 511; DB
Pred. No. 2.2e
7; Mismatches
                                                                                                                                                                                                                      γď
                                                                                                                                                                                                                                             by ccs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                ₽
                                                                                                                                                                                                                                                                 by GGW"
                                                                                                                                                                                                                         TCR"
                                                                                                                                                                                                                                                                                         GGY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 23;
.2e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   574
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RESULT 7
AAY32074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents rapessed raffinose synthase, a protein that can bind a D-galactosyl group through an alpha(1-6) bond to the hydroxy group attached to the carbon atom at the 6-position of the D-glucose residue in a sucrose molecule to form raffinose. cDNA (see AAZ20210) encoding the enzyme was isolated from rapessed cv. Westar leaf cDNA by PCR. Probes or primers generated from plant raffinose synthase genes (see AAZ20207-10) may be used to obtain other raffinose synthase genes by labeled detection or amplification (claimed). These genes may be used to control the levels of raffinose produced in plants. Antisense genes to increase the level of gene activity. The resulting transgenic plants may be used as a food source to alter the growing conditions for gut enterobacteria, or providing general health advantages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                           30-APR-1998;
30-APR-1998;
04-DEC-1998;
10-DEC-1998;
     New
                                    N-PSDB; AAZ20209
                                                                                        Watanabe
                                                                                                                                                                                                                                                                                    03-NOV-1999
                                                                                                                                                                                                                                                                                                                    EP953643-A2
                                                                                                                                                                                                                                                                                                                                                                                                                       Brassica juncea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mustard raffinose synthase.
                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Raffinose synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY32074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY32074 standard; Protein; 777
                                                                                                                       (SUMO ) SUMITOMO CHEM CO LTD
                                                                                                                                                                                                                                                 27-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New sense and antisense genes, useful for altering the level of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       μ
     sense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1999-593144/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; 88
                                                                                 Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
   and antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 36-38; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            572 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
                                                                                        0eda
                                                                                                                                                           98JP-0120550.
98JP-0120551.
98JP-0345590.
98JP-0351246.
                                                                                                                                                                                                                                                 99EP-0107430
                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 210
                                                                                                                                                                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                         mustard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.1%;
87.1%;
                                                                                                                                                                                                                                                                                                                                                   "encoded by ACR"
genes, useful for altering
                                                                                                                                                                                                                                                                                                                                                                                                                                                         transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 508; DB 20; Pred. No. 3.4e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 572;
 the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
 level
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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RESULT 8
AAW57886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
This sequence represents the broad bean raffinose synthetase of the invention. The raffinose synthetase is capable of producing raffinose combining a D-galactosyl group through an alpha (1-6) bond with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (claimed). These genes may be used to control the levels of raffinose produced in plants. Antisense genes can be used to knock out existing gene activity, and sense genes to increase the level of gene activity. The resulting transgenic plants may be used as a food source to alter the growing conditions for gut enterobacteria, providing general health advantages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D-glucose residue in a sucrose molecule to form raffinose. cDNA (see AAZ20209) encoding the enzyme was isolated from mustard (Brassica juncea) leaf cDNA by PCR. Probes or primers generated from plant raffinose synthase genes (see AAZ20207-10) may be used to obtain other raffinose synthase genes by labeled detection or amplification
                                                      Claim
                                                                           capable of producing raffinose, used as food
beneficial effects on gastrointestinal flora
                                                                                          New nucleic acid molecule encoding plant raffinose capable of producing raffinose, used as food additi
                                                                                                                                                 WPI; 1998-324670/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents mustard raffinose synthase, a protein that can bind a D-galactosyl group through an alpha(1-6) bond to the hydroxy group attached to the carbon atom at the 6-position of the
                                                                                                                                     N-PSDB; AAV40800
                                                                                                                                                                          Oeda K,
                                                                                                                                                                                                                                                                                    24-JUN-1998
                                                                                                                                                                                                                                                                                                             EP849359-A2
                                                                                                                                                                                                                                                                                                                                      Vicia
                                                                                                                                                                                                                                                                                                                                                                 gastrointestinal flora; broad bean.
                                                                                                                                                                                                                                                                                                                                                                          Raffinose synthetase; metabolism modification; food
                                                                                                                                                                                                                                                                                                                                                                                                        Broad
                                                                                                                                                                                                                                                                                                                                                                                                                                 23-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW57886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW57886 standard;
                                                                                                                                                                                                    (SUMO)
                                                                                                                                                                                                                              18-DEC-1996;
                                                                                                                                                                                                                                                        18-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 PDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1:
                                                                                                                                                                                                                                                                                                                                      faba.
                                                                                                                                                                                                                                                                                                                                                                                                      bean raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88;
                                                                                                                                                                                                     SUMITOMO CHEM CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                    Page 26-29;
                                                                                                                                                                          Wantanabe E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              777 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      food plants
                                                                                                                                                                                                                               96JP-0338673
                                                                                                                                                                                                                                                        97EP-0122417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
                                                   44pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.7%;
87.1%;
                                                                                                                                                                                                                                                                                                                                                                                                      synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55pp;
                                                    English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 506; DB Pred. No. 9.4e 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.4e-56;
                                                                                          finose synthetase additives with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                             additive;
  y raffinose
with a
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RESULT 9
AAY30142
AAY30142
AAY301A2
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Best Local Similarity
                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule. The DNA can be used to modify metabolism of a host organism by introducing into the host organism or its cell so that the content of the raffinose family oligosaccharides in the host organism or cell is changed. Raffinose oligosaccharides are useful as food additives with beneficial effects on the gastrointestinal flora.
                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a raffinose synthase protein. The sequence is isolated from plant material of broad beans. The protein forms raffinose by complexing alpha(1 to 6). D-galactosyl hydroxyl group of the 6C of D-glucose residue in sucrose molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New raffinose synthase gene - is prepared from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-511112/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-NOV-1997;
18-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vicia faba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Raffinose synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY30142;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SUMO ) SUMITOMO CHEM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       529
  589
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                                               61
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                                                                                            PDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLYLPDGSILRSEYYALP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWC 100
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                       TRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWC 100
TRDCLFEDPLHNGKTMLKIWNLNKYTGVLGLFNCQGGGWC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; 88
                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ10001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 19-21; 40pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          799 AA;
                                                                                                                                                                                                                                                                                                    799 AA;
                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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96JP-0338673.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of a raffinose synthase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89.5%;
                                                                                                                                                                                                                           89.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           799
                                                                                                                                                                                                Score 505; DB 20;
Pred. No. 1.3e-55;
5; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 505; DB 19;
Pred. No. 1.3e-55;
5; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bean;
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  628
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                                                                                                                                                                                                                                                Length 799;
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                                                                                                                                                                                                Gaps
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RESULT 10
AAB98659
ID AAB98
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AAW57887
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                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                             The present invention relates to a mutant protein of raffinose synthas in which at least one aromatic amino acid present at the position of about 1-7 amino acids from the N-terminus is deleted or replaced. The mutant protein can be used for reducing the raffinose oligosaccharide content in a plant body. The present protein from soybean, was used in the present inventor in the present protein from soybean, was used in the present in a plant body.
                           Glycine max
                                                                                                                                          AAW57887
                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                        the
                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                Novel mutant protein of raffinose synthase is useful for reducing the raffinose oligosaccharide content in a plant body \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-JUL-2000; 2000JP-0200571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plant; soybean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mutant; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Soybean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB98659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB98659 standard; protein; 780 AA.
        EP849359-A2
                                                gastrointestinal flora;
                                                       Raffinose synthetase;
                                                                            Soybean raffinose synthetase.
                                                                                                  23-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SUMO ) SUMITOMO CHEM
                                                                                                                                                                                            570
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                                                                                                                                                                                                               TRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWC 100
                                                                                                                                                                                          max.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH27438
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                                                                                                                                          standard; Protein;
                                                                                                                                                                                                                                                                                                                   780 AA;
                                                                                                                                                                                                                                                                                                                                                                                                            Page 18-20; 30pp; Japanese.
                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                        invention
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                                                                                                                                                                                                                                                                                     88.3%;
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                                                         metabolism
                                               soybean
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                                                                                                                                          781 AA
                                                                                                                                                                                                                                                                                    Score 498; DB 2
Pred. No. le-54;
                                                                                                                                                                                                                                                                            Mismatches
                                                         modification;
                                                                                                                                                                                                                                                                                               22;
                                                                                                                                                                                            609
                                                         food additive;
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
New raffinose synthase
                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents the soybean raffinose synthetase of the invention. The raffinose synthetase is capable of producing raffinose by combining a D-galactosyl group through an alpha (1-6) bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule. The DNA can be used to modify metabolism of a host organism by introducing into the host organism or its cell so that the content of the raffinose family oligosaccharides in the host organism or cell is changed. Raffinose oligosaccharides are useful as food additives with beneficial effects on the gastrointestinal flora.
                                                                                                                                                                                    28-NOV-1997;
18-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                        JP11215984-A
                                                                                                                                                                                                                                                                                                                                                                                                                            Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of a raffinose synthase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY30143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY30143 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Raffinose synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid molecule encoding plant raffinose synthetase capable of producing raffinose, used as food additives with beneficial effects on gastrointestinal flora
                                                                                                                                   (SUMO ) SUMITOMO CHEM
                                                                                                                                                                                                                                                                12-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 31-34; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAV40801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0eda
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                                                                                                                                                                                                                                                                                                                    10-AUG-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SUMO ) SUMITOMO CHEM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                 1999-511112/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRDCLFEDPLHDGKTMLKIWNLNKYTGVLGLFNCQGGGWC 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDWDMFQSTHPCAAFHAASRAISGGFIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDWDMFQSTHPCAEFHAASRAISGGPVYVSDCVGKHNFKLLKSLALPDGTILRCQHYALP 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1998-324670/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85;
                                                         AAZ10002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wantanabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            781 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                                                                                                                                                    97JP-0329006.
96JP-0338673.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plant; sucrose; raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.1%;
                                                                                                                                   CO LTD
gene
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prepared
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1.4e-54;
hes 7;
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plant material
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
                                         Query Match
Best Local Similarity
Matches 85; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                              with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a raffinose synthase protein. The sequence is isolated from plant material. The protein forms raffinose by complexing alpha(1 to 6)- D-galactosyl hydroxyl group of the 6C of D-glucose residue in sucrose molecules.
                                                                                     Sequence
                                                                                                                     The present invention provides novel plant promoters which can be the production of transgenic plants which express genes with desir
                                                                                                                                                                                 New soybean plant promoters useful for generating transgenic with desired properties
                                                                                                                                                                                                                                                                                          30-APR-1999;
01-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                           Glycine
                                                                                                           properties.
                                                                                                                                                     Example 6; Page 24-27;
                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                              Ishige F,
                                                                                                                                                                                                                                                                                                                         27-APR-2000; 2000EP-0108962
                                                                                                                                                                                                                                                                                                                                                02-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                      EP1048733-A2
                                                                                                                                                                                                                                                                                                                                                                                                                 Plant promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Soybean raffinose synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB49400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB49400 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 8; Page 25-27; 40pp; Japanese
                                                                                                                                                                                                                                                                    (SUMO ) SUMITOMO CHEM CO LTD.
511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 PDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALP 60
PDWDMFQSTHPCAEFHAASRAISGGPVYVSDCVGKHNFKLLKSLALPDGTILRCQHYALP
           PDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALP
                                                                                                                                                                              desired
                                                                                                                                                                                                              2001-104537/12.
DB; AAC89523.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDWDMFQSTHPCAEFHAASRAISGGPVYVSDCVGKHNFKLLKSLALPDGTILRCQHYALP 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                              Watanabe E,
                                                                                       781 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               781 AA;
                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                           properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                          99JP-0124527.
99JP-0247211.
                                                                                                                                                                                                                                                                                                                                                                                                               transgenic plant; desired property.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                     88.1%;
85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.1%;
85.0%;
                                                                                                                                                      36pp;
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                                         Score 497; DB
Pred. No. 1.4e
8; Mismatches
                                          8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       781
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                                                                                                                                                      English
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Pred. No. 1.4e-54;
8; Mismatches 7;
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                                                    DB 22;
L.4e-54;
                                                               Length 781;
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                                          Indels
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                                            0;
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                                         Gaps
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 570
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RESULT 15
AAY32073
ID AAY32
XX
AC AAY32
AC AAY32
XX
DT 17-JA
XX
DE Sugar
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AAY70978
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                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                             The present sequence is a raffinose synthase from clone sfl1.pk125.d4 isolated from a soybean immature flower cDNA library sfl1. Raffinose synthase is involved in the biosynthesis of raffinose and higher homologues in the raffinose saccharide family from sucrose. The present sequence is useful for reducing the raffinose saccharide content of soybean seeds which improves the nutritional quality of the soy protein products derived from them.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids and encoded proteins involved in the biosynthesis of raffinose, useful for producing soybean seeds with a reduced raffinose content and therefore improved nutritional quality -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycine
           Sugarbeet raffinose synthase
                                   17-JAN-2000
                                                           AAY32073
                                                                                AAY32073 standard; Protein;
                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 47-49; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-350754/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Allen SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (DUPO ) DU PONT DE NEMOURS &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200024915-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Soybean; raffinose synthase; raffinose saccharide; clone sfll.pkl25.d4; nutritional; soy protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Soybean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-2000
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                                                                                                                                             547
                                                                                                                                                                                           487
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                                                                                                                                                                                                                                                    Local
                                                                                                                                                        TRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWCR 101
                                                                                                                                                                                                      PDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALP 60
                                                                                                                                          TRDCLFADPLHDGKTMLKIWNINKYTGVLGVFNCQGGGWFR 587
                                                                                                                                                                                        PDWDMFQSTHPCAAFHAASRAISGGPIYISDTVGNHNFELLKTLALPDGSILRCEHYALP 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      max.
                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hitz WD;
                                                                                                                                                                                                                                                                                       758 AA;
                                                                                                                                                                                                                                         Conservative
                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0105451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US24923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               synthase from clone sfll.pkl25.d4
                                                                                                                                                                                                                                                   87.6%;
                                                                                 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        758
                                                                                                                                                                                                                                         9;
                                                                                                                                                                                                                                      Score 494; DB 21;
Pred. No. 3.2e-54;
9; Mismatches 7;
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                                                                                                                                                                                                                                                              Length 758;
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Search completed: March Job time: 72.439 secs

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                                                                                                      Query Match
Best Local S
Matches 84
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30-APR-1998;
04-DEC-1998;
                                                                                                                                                                                 haming leaf cDNA by PCR. Probes or primers generated from plant raffinose synthase genes (see AAZ20207-10) may be used to obtain other raffinose synthase genes by labeled detection or amplification (claimed). These genes may be used to control the levels of raffinose produced in plants. Antisense genes can be used to knock out existing gene activity, and sense genes to increase the level of gene activity. The resulting transgenic plants may be used as a food source to alter the growing conditions for gut enterobacteria, providing general health advantages.
                                                                                                                                                                                                                                                                                                   This sequence represents sugarbeet raffinose synthase, a protein that can bind a D-galactosyl group through an alpha(1-6) bond to thydroxy group attached to the carbon atom at the 6-position of the D-glucose residue in a sucrose molecule to form raffinose. CDNA (see AAZ22208) encoding the enzyme was isolated from sugarbeet cv.
                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAZ20208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Watanabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                            New sense and antisense genes, useful for altering the level
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SUMO ) SUMITOMO CHEM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Raffinose synthase; sugarbeet; transgenic plant.
 570
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TKDCLEVDPLHDGKTMLKIWNLNKYNGVLGVFNCQGGGWSR
                          TRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWCR 101
                                                                 PDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vulgaris
                                                                                                                                                                                                                                                                                                                                                                                     25; Page 22-24;
                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 in
                                                                                                                                                          783 AA;
                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               food plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oeda K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98JP-0120551
98JP-0345590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99EP-0107430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98JP-0351246
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348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "encoded by CCR'
                                                                                                                  84.4%;
                                                                                                                                                                                                                                                                                                                                                                                    55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "encoded by
                                                                                                                  Score 476; DB 20;
Pred. No. 6.8e-52;
                                                                                                         Mismatches
 610
                                                                                                                               Length 783;
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/P

2: /cgn2_6/ptodata/2/pubpaa/U

3: /cgn2_6/ptodata/2/pubpaa/U

4: /cgn2_6/ptodata/2/pubpaa/U

6: /cgn2_6/ptodata/2/pubpaa/U

5: /cgn2_6/ptodata/2/pubpaa/U

6: /cgn2_6/ptodata/2/pubpaa/U

7: /cgn2_6/ptodata/2/pubpaa/U

9: /cgn2_6/ptodata/2/pubpaa/U

10: /cgn2_6/ptodata/2/pubpaa/U

11: /cgn2_6/ptodata/2/pubpaa/U

11: /cgn2_6/ptodata/2/pubpaa/U
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Gapop 10.0 , Gapext 0.5
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/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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US-09-815-837-41	US-09-815-837-17	US-10-078-770-102	US-09-960-226-4	US-09-847-172-44	US-10-054-295-55	US-10-053-758-55	US-09-438-486-55	US-09-766-253-55	US-09-843-676-55	US-10-081-281-93	US-10-047-539-2	US-09-801-368-148	US-10-043-487-266	US-09-815-242-5100	US-09-738-626-4624	US-09-847-172-23	US-09-858-580-23	ID
Sequence 41, App.	Sequence 17, Appl	Sequence 102,	Sequence 4, Appli	Sequence 44, A	Sequence 55, A	Sequence 55, A	Sequence 55, A	Sequence 55, Ap	Sequence 55, Appl	Sequence 93, 1	Sequence 2, Appli	Sequence 148, App	Sequence 266, App	Sequence 5100, Ap	Sequence 4624,	Sequence 23, Appl	Sequence 23, Ap	Description

RESULT 2 US-09-847-172-23 : Sequence 23, Application US/09847172 : Publication No. US20030007978A1

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	10000000000000000000000000000000000000
	380 3175 323 323 323 323 323 445 453 445 336 445 336 445 337 537 537 537
ALIGNMENTS	US-09-934-900-12 US-09-989-919-84 US-10-078-770-118 US-10-778-770-116 US-09-977-260-12 US-09-977-260-12 US-09-977-260-12 US-09-915-32-13951 US-10-108-605-185 US-09-815-837-13 US-09-815-837-13 US-09-815-837-27 US-09-815-837-27 US-09-815-837-27 US-09-815-837-27 US-09-815-837-27 US-09-815-837-27 US-09-815-837-27 US-09-915-837-27 US-09-915-837-37 US-09-915-837-37 US-09-915-837-37 US-09-915-837-37 US-09-915-837-37 US-09-915-837-37 US-09-915-837-37 US-09-915-837-37 US-09-915-837-37 US-09-977-260-11
	Sequence 12, Appl Sequence 108, App Sequence 116, App Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 13, Appl Sequence 185, Appl Sequence 185, Appl Sequence 1951, A Sequence 1096, Ap Sequence 1, Appl Sequence 1, Appl Sequence 23, Appl Sequence 25, Appl Sequence 37, Appl Sequence 37, Appl Sequence 25, Appl Sequence 25, Appl Sequence 11, Appl Sequence 213, Appl Sequence 213, Appl

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RESULT 1
US-09-858-580-23
; Sequence 23, Application US/09858580
; Patent No. US20020178864A1
; GENERAL INFORMATION:
; APPLICANT: Burrows et al.
; TITLE OF INVENTION: Recombinant MHC molecules useful for manipulation of TITLE OF INVENTION: antigen-specific T-Cells
; FILE REFERENCE: 48823
; FILE REFERENCE: 48823
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; ORGANISM: Mus sp
US-09-858-580-23
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CURRENT EILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 09/153,586
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/064,552
PRIOR APPLICATION NUMBER: 60/064,552
PRIOR FILING DATE: 1997-09-16
PRIOR APPLICATION NUMBER: 60/064,555
PRIOR FILING DATE: 1997-10-10
NUMBER OF SEQ ID NOS: 30
                                                                                                                                            Query Match 25.2
Best Local Similarity 26.2
Matches 21; Conservative
                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver.
SEQ ID NO 23
LENGTH: 174
132 -- IWRLEEF-AKFASFEAQG 148
                                     ·77 LKIWNLNKFTGVIGAFNCQG 96
                                                                                                           31 DSVGKHNEDLLKKLVLP----DGSILRSEYYALPTR------DCLFEDPLHNGETM 76
                                                                            73
                                                                            DTVCRHNYEIFDNFLVPRRVEEHTIIQAEFYLLPDKRGEFMFDFDGDEIFHVDIEKSET- 131
                                                                                                                                                                       15.1%;
26.2%;
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                                                                                                                                                      Score 85; DB
Pred. No. 0.02
L8; Mismatches
                                                                                                                                                                             DB 9;
0.022;
                                                                                                                                                          23;
                                                                                                                                                                                              Length 174;
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; ORGANISM: Corynebacterium glutamicum US-09-738-626-4624
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                                                                                                                                    SOFTWARE: PatentIn ver.
SEQ ID NO 4624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.1 SEQ ID NO 23
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                      PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-09
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEO ID NOS: 7059
                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: JP 99/377484 PRIOR FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/847,172 CURRENT FILING DATE: 2001-05-01 PRIOR APPLICATION NUMBER: US 60/200,942 PRIOR FILING DATE: 2000-05-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: RECOMBINANT MHC MOLECULES USEFUL FOR MANIPULATION OF ANTIGEN-SPECTITLE OF INVENTION: CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1997-09-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 09/153,586 PRIOR FILING DATE: 1998-09-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: OREGON HEALTH AND SCIENCES UNIVERSITY APPLICANT: BURROWS, GREGORY G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 899-58137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: VANDENBARK, ARTHUR A.
                                                                                                   TYPE: PRT
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                                                                                                                    ENGTH: 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 DTVCRHNYEIFDNFLVPRRVEEHTIIQAEFYLLPDKRGEFMFDFDGDEIFHVDIEKSET- 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 LKIWNLNKFTGVIGAFNCQG 96
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YOKOI, HARUHIKO
TATEISHI, NAOKO
                                                                                                                                                                                                                                                                                                                                                                                              OZAKI, AKIO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAYASHI, MIKIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANDO, SEIKO
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                                                                                                                                                                                                                                                                                                                                                                                                                IKEDA, MASATO
  12.2%;
27.6%;
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  Score
Pred.
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  No.
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. 0.022;
  DB 9;
4.8;
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                  Length 426
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US-10-043-487-266
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                                                                                                                                                      Sequence 266, Applic Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ
SEQ ID NO 5100
LENGTH: 183
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                                                        TITLE OF INVENTION: Protein-protein interactions between Shigella Flexneri polypep TITLE OF INVENTION: mammalian polypeptides FILE REFERENCE: B4778A
                                                                                                                                                                                                                                                                                                                                                                                             Best
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CURRENT APPLICATION NUMBER: US/10/043,487
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/261,130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: APPLICANT:
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                                                                                                                    APPLICANT: HYBRIGENICS APPLICANT: Pierre, LEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/242,578
PRIOR TILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NICURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Identification of Essential Genes TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-12-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/207,727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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                                                                                                                                                                                                                                                                                           94 LFQATNPSAAGNLVNTAASGATGVALQLLDSVGGNPVDLAGGAAVPAGDIV 144
                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 ETMLKIWNLNKFTGVI 89
                                                                                                                                                                                                                                                                                                                                 5 MFQSTHPCAAFHAASRAISGG---PIYVSDSVGKHNFDLLKKLVLPDGSIL 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/815,242
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                                                                                                                    Pierre, LEGRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamamoto, Robert T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zyskind, Judith W.
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                                                                                                                                                                          Application US/10043487 o. US20030055220A1
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Pred. No. 2;
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RESULT 7
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Sequence 2, Application US/10047539 Patent No. US20020177547A1
                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.0
SEQ ID NO 148
LENGTH: 358
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.1
SEQ ID NO 266
LENGTH: 1138
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/160,587
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
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                                                                                                                                                                      186
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                                                                                                    236 ELSETP-----LMRFAGVFEFMNC
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                                                                                                                                     64 CLEEDPLHNGETMLKIWNLNKETGVIGAENC 94
                                                                                                                                                                                                    15 FHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSI-----LRSEYYAL----PTRD 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45 --- VLPDGSILRSEYYALPTRDCLFEDPLHNGETMLKI 79
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                                                                                                                                                                   FHA-----YQTANFLQENFEAIKKVVCPDSCLQHQQRQPKRPKRYSLLLLIPNAS 235
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Madden, Kevin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salama, Sofie
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US20020128250Alman,
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26.5%;
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Pred. No. 27;
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Pred. No. 13;
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US-10-081-281-93
; Sequence 93, Application US/10081281
; Patent No. US20020151707A1
; GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/10/047,539
CURRENT FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: EP 01 10 0914.9
PRIOR FILING DATE: 2001-01-16
NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS FOR TREATING OR PREVENTING TITLE OF INVENTION: CANCER
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                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sheppard, Paul TITLE OF INVENTION: Immune Mediators and Related Methods NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kindsvogel, Wayne
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NAWRATH, MICHAEL
NAME: Parent,
                                        APPLICATION NUMBER: US 60/005,964 FILING DATE: 27-CCT-1995 APPLICATION NUMBER: US 08/657,581 FILING DATE: 07-JUN-1996
                                                                                                                            APPLICATION NUMBER: US 08/483,241 FILING DATE: 07-JUN-1995
                                                                                                                                                                    APPLICATION NUMBER: US/09/261,811A
FILING DATE: 03 Mar-1999
APPLICATION NUMBER: US 08/480,002
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/482,133
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/081,281 FILING DATE: 20-Feb-2002
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24.88;
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Pred. No. 26;
17; Mismatches
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TOPOLOGY: linear;
; MOLECULE TYPE: protein;
; SEQUENCE DESCRIPTION: SEQ ID NO: US-10-081-281-93
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Best Local
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                   TELECOMMUNICATION INFORMATION
                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
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19; Conser
                                                                                                                   APPLICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997 APPLICATION NUMBER: US 08/844,419 FILING DATE: 18-APR-1997 APPLICATION NUMBER: US 08/724,643 FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/843,676 FILING DATE: 26-Apr-2001 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                         NAME: Apple, Randolph T. REGISTRATION NUMBER: 36,429
                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/854,050 FILING DATE: 09-MAY-1997
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TELEFAX: (415) 576-0300
TELEPHONE:
                                        REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Two Embarcadero Center, 8th Floor
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Harley, Calvin
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Chapman, Karen B.
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Pred. No. 8.8;
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US-09-766-253-55
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                                                                                                                          INFORMATION FOR SEQ ID NO: 55: SEQUENCE CHARACTERISTICS:
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SEQUENCE CHARACTERISTICS:
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nes 23; Conserv
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,253
                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/724,643 FILING DATE: 01-OCT-1996 ATTORNEY/AGENT INFORMATION:
MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 55:
                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
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ADDRESSEE: Townsend and Townsend and Crew LLP
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                                                                                                                                                                                                                        NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/846,017 FILING DATE: 1997-04-25
                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 19-Jan-2001 CLASSIFICATION: <Unknown>
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STATE: California
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                                        TOPOLOGY: not relevant
                                                                STRANDEDNESS: not relevant
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                                                                                                       LENGTH: 884 amino acids
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Harley, Calvin
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Chapman, Karen B.
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29.5%;
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Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                           FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 01-QCT-1996
CLASSIFICATION: 536
                                                       TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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STATE: Co...
COUNTRY: United
TD: 94111-3834
TD: PRADABLE F
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APPLICANT:
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CLASSIFICATION: 53b
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
APPLICATION NUMBER: 18-APR-1997
77 TMC DATE: 18-APR-1997
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002931US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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PRIOR APPLICATION DATA:
PRIOR TARTON NUMBER: US 08/846,017
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APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
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APPLICATION NUMBER: US/0:
FILING DATE: 12-00/-1999
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APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. US20030009019Alel Telomerase
NUMBER OF SEQUENCES: 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 0 FILING DATE: 25-APR-1997
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CITY: San Francisco
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 STRANDEDNESS:
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                                     ENGTH:
                     amino acid
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Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
                                       884 amino acids
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not relevant
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; TOPOLOGY: not releval ; MOLECULE TYPE: peptide US-09-438-486-55
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US-10-053-758-55
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Best Local S
Matches 23
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                                                                                                                                 INFORMATION FOR SEQ ID NO: 55: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 PIYVSDSVGKHNFDLLKKL--VLPDGSIL----RSEYYALPTRDC--LFEDPL--HNGET 75
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Local Similarity 29.5%;
nes 23; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Andrews, William H.
TITLE OF INVENTION: NO. US20030032075Alel Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                               TELECOMMUNICATION INFORMATION
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 55:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                       NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/844,419 FILING DATE: 18-APR-1997 APPLICATION NUMBER: US 08/724,643 FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/854,050 FILING DATE: 09-MAY-1997 APPLICATION NUMBER: US 08/851,843 FILING DATE: 06-MAY-1997 APPLICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997 FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                       STRANDEDNESS: No. US20030032075A1 Relevant
                                                                                     TYPE: amino acid
                                                                                                                                                                             TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
                                                                                                          LENGTH: 884 amino acids
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Morin, Gregg B.
Harley, Calvin
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Nakamura, Toru
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Pred. No.
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SEQUENCE DESCRIPTION: SEQ ID NO: US-10-054-295-55
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US-10-054-295-55
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     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                              TELEFAX: (415) 576-0 INFORMATION FOR SEQ ID NO: 55:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: No. US20030044953Alel Telomerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                      NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                  STRANDEDNESS: No. US20030044953A1 Relevant TOPOLOGY: No. US20030044953A1 Relevant
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/844,419 FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/854,050 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/10/054,295 FILING DATE: 18-Jan-2002
                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/724,643 FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
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                                                                                                                                                                          LENGTH: 884 amino acids
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Nakamura, Toru
Chapman, Karen B.
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Harley, Calvin
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       11.2%;
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Pred. No.
       Score
Pred.
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       No.
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. 59;
DB
59;
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                       9;
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                       Length 884;
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; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-172-44
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CURRENT FILING DATE: 2001-05-01
PRIOR APPLICATION NUMBER: US 60/200,942
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 09/153,586
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: US 60/064,555
PRIOR FILING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: US 60/064,552
PRIOR FILING DATE: 1997-09-16
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                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09960226 Patent No. US20020172670A1
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                                                                                        APPLICANT: Rose, David
APPLICANT: Kuntz, Douglas
APPLICANT: Van Den Elsen, Jean
APPLICANT: Van Den Elsen, Jean
TITLE OF INVENTION: MANNOSIDASE STRUCTURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: VANDENBARK, ARTHUR A.
TITLE OF INVENTION: RECOMBINANT MHC MOLECULES USEFUL FOR MANIPULATION OF ANTIGEN-S
TITLE OF INVENTION: CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: APPLICANT:
                                   SOFTWARE: PatentIn version 3.1
                                                      PRIOR FILING DATE: 2000-09-22 NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 899-58137
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LENGTH: 1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 T---VWRLEEF-GRFASFEAQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75 TMLKIWNLNKFTGVIGAFNCQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 DSVGKHN-----FDLLKKLVLPDGSILRSEYYALPTR------DCLFEDPLHNGE 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 MLKIWNLNKFTGVIGAFN 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 PIYVSDSVGKHNFDLLKKL--VLPDGSIL----RSEYYALPTRDC--LFEDPL--HNGET 75
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23.2%; Pred. No.
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13;
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9: sp_phage:*
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4225
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ALIGNMENTS

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121 ILEKSDSGRPYVFLLPIVEGPFRTSIQPGDDDFVDVCVESGSSKVVDASFRSMLYLHAGD 180 	61 PVSVGCFVGFDASEPDSRHVVSIGKLKDIRFMSIFRFKVWWTTHWVGRNGGDLESETQIV 120 	MAPSFKNGGSNVVSFDGLNDMSSPFAIDGSDFTVNGHSFLSDVPENIVASPSPYTSIDKS 60	Query Match 100.0%; Score 4225; DB 10; Length 784; Best Local Similarity 100.0%; Pred. No. 0; Matches 784; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Glycosyltransferase; Transferase. SEQUENCE 784 AA; 86920 MW; 3B06A491F0908933 CRC64;	Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases. EMBL; $AF073744$; $AAD02832.1$;	Ohsumi C., Nozaki J., Kida T.;	SEQUENCE FROM N.A.	[1]	eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;	Cucumis sativus (Cucumber). Rukarvota: Viridinlantae: Strentonhuta: Emhruonhuta: Tracheonhuta:	RFS.		01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)	Ol-MAY-1999 (TrEMBLrel. 10, Created)	Q92T62 PRELIMINARY; PRT; 784 AA.	LT 1 62

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                           Tabata S.;
"Structural analysis of Arabidopsis
"Sequence features of the regions of
physically assigned Pl clones.";
DNA Res. 4:291-300(1997).
[2]
                                                                                STRAIN-COLUMBIA;
STRAIN-COLUMBIA;
MEDLINE-98069011; PubMed-9405937;
MEDLINE-98069011; Sato S.,
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

PR EMBL; AB006702; BaB11595.1; -

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OBVWN6;
O1-MAR-2002 (TrEMBLre1. 20
O1-MAR-2002 (TrEMBLre1. 20
O1-MAR-2002 (TrEMBLre1. 20
TremBlre1. 20
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SEQUENCE 798 AA; 88717 MW; 8D3F3ED5BF8617B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CV. WUNDER VON KELVEDON; TISSUE-SEED; Peterbauer T., Mach L., Mucha J., Richter A., Peterbauer T., Mach L., Mucha J., Richter A., Peterbauer T., Mach L., Mucha J., Richter Synthase from "Molecular characterization of raffinose synthase from sativum L.) seeds.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoldeae; Vicieae; Pisum.
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SVGKHNEDLLKKLVLPDGSILRSEYYALPTRDCLFEDPLHNGETMLKIWNLNKFTGVIGA
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510; Conserv
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. 20, Last sequence update)
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2.4.1.82).
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RESULT 4
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Q942T6; O1-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                  Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases EMBL; AP003282; BAB64768.1; - SEQUENCE 816 AA; 89588 MW; B316EDF3566C5178 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lilliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                      LKFQENYKFRDYVNPKATGPRAGQKGMKAFIDELKGEFKTVEHVYVWHALCGYWGGLRPQ 343
                                                                                       TVHPQGVIEGVRHLVDGGCPPGLVLIDDGWQSIGHDSDPITK--EGMNQTVAGEQMPCRL
                                                                                                                                         VDASFRSMLYLHAGDDPFALVKEAMKIVRTHLGTFRLLEEKTPPGIVDKFGWCTWDAFYL 225
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VPGLPEARVIQPVLSPGLQMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGID
                                                                            KVHPEGVWEGVRRLADGGCPPGLVLIDDGWQSICHDDDDLGSGAEGMNRTSAGEQMPCRL
                                                                                                                                                                               VENETQMMILDQSGTKSSPTGPRPYVLLLPIVEGPFRACLESGKAEDYVHMVLESGSSTV
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                         IKFQENYKFREY-----KGGMGGFVREMKAAFPTVEQVYVWHALCGYWGGLRPG
                                                                                                                            RGSVFRSAVYLHAGDDPFDLVKDAMRVVRAHLGTFRLMEEKTPPPIVDKFGWCTWDAFYL
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59.68;
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                                                                                                                                                                                                                                                                                                                                  Score 2643; DB 10;
Pred. No. 2.1e-206;
1; Mismatches 150;
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Best Local S
Matches 379
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosid eurosids I; Fabales; Fabaceae; Papillonoideae; Vicieae; Pisum.
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-MAR-2002 (TrEMBLrel. 20, Last annotation
stachyose synthase (EC 2.4.1.67).
                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases EMBL; AJ311087; CAC38094.1; -. Glycosyltransferase; Transferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peterbauer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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ELTLEPFTYELLVVAPVRAIVSPELGIGFAPIGLANMLNAGGAVQGFEAARKDGDVAA-E
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IGKSGSDLQMETQWILLIEVPET-KSYVVIIPIIEKCFRSALFPGFNDHVKIIAESGSTKV
                                              VGRNGGDLESETQIVILEKSDSGRPYVFLLPIVEGPFRTSIQPGDDDFVDVCVESGSSKV 165
                                                                                                SESNAPPSLLQKVLAYSHKGGFFGFSHETPSDRLMNSIGSFNGKDFLSIFRFKTWWSTQW
                                                                                                                                                                                                  MAPPLNSTTSNLIKTESIFDLSE-----RKFKVKGFPLFHDVPENV--SFRSFSSICKP
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                                                                                                                                                                                                                                                                                                                                                                                                        853 AA;
                                                                                                                                                                                                                                                                                                     Conservative 147;
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Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAY-2000 (TrEMBLrel. 20, Last annotation update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Galactinol-raffinose galactosyltransferase (EC 2.4.1.67).
Phaseolus angularis (Adzuki bean) (Vigna angularis).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Roside eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
QCBI_TaxID=3914;
              molecular cloning and functional plant J. 20:509-518(1999).
EMBL; Y1024; Ch864363.1; -.
Glycosyltransferase; Transferase.
                                                    SEQUENCE FROM N.A.
MEDLINE=20117502; PubMed=10652123;
Peterbauer T., Mucha J., Mayer U., Popp M., Gloessl J., Richter Peterbauer T., Mucha J., Mayer U., Popp M., Gloessl J., Richter "Stachyose synthesis in seeds of adzuki bean (Vigna angularis):
"Stachyose synthesis in seeds of adzuki bean (Vigna angularis):
                                                                                                                                                                                                                                                                                                                      Q9SBZ0
                                                                                                                         SEQUENCE FROM N.A.
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AA;
94949
MW;
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RESULT 7

QBRW08

ID QBRW08

AC QBRW08;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
E Stachyose synthase (EC 2.4.1.67).
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Pred. No. 5.8e-147;
39; Mismatches 243;
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stachys sieboldii.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ database
EMBL; AJ344091; CAC86963.1;
Transferase; Glycosyltransferase.
SEQUENCE 863 AA; 95227 MW; DD96FE666099DEFD CRC64;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Lamiales; Lamiaceae; Stachys.
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                                                         NPISIEGVKTFALYLYQAKKLILSKPSQD-LDIALDPFEFELITVSPVTKLIQTSLHFAP
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366; Conser
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Pred. No. 3e-1,
.43; Mismatches
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Q9SYJ4;
01-MAY-2000
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Putative raffinose synthase OR seed IMBIBITION pro
T7B11.23 OR AT4G01970
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophy
Spermatophyta; Magnoliophyta; eudicotyledons; corrections II; Brassicales; Brassicaceae; Arabidops
                                                                                                                                                                                                                                                                                                                                                                                                  EU Arabidopsis sequencing px
Submitted (MAR-2000) to the
EMBL; AC007138; AAD22659.1;
EMBL; ALL61493; CAB80690.1;
SEQUENCE 807 AA; 90122 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Huang E.N., Nascimento L., de la Bastide M., Habermann K., Preston R.R., Spiegel L.A., See L.H., Shah R., Matero A., O'Shaughnessy A., Rodriguez M., Shekher M., Swaby I., Schutt Parnell L.D., Dedhia N.N., McComble W.R.;
"Arabidopsis thaliana BAC T7B11 from chromosome IV near 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M., Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M., Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N., Mewes H.W., Lemcke K., Mayer K.F.X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=CV. COLUMBIA;
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                                                                                                 MAPSFKNGGSNVVSFDGLNDM--SSPFAI-------DGSDFTVNGHSFLSDV
IVDKFGWCTWDAFYLTVHPQGVIEGVRHLVDGGCPPGLVLIDDGWQSIGHDSDPITKEGM
                                                                                                                                                                              SIFRFKVWWTTHWVGRNGGDLESETQIVILE--KSDSGRPYVFLLPIVEGPFRTSIQPGD
                                                                                                                                                             SLFRFKMWWSTAWIGKSGSDLQAETQWVMLKIPEIDS----YVAIIPTIEGAFRASLTPGE
                                                                                                                                                                                                                      PONVTFTPFSSHSISTDAPLPILLRVQANAHKGGFLGFTKESPSDRLTNSLGRFEDREFL
                                                                                                                                                                                                                                                                                MAPLHE-----SLSSINDVIESKPLFVPITKPILQPNSFNLSEGSLCAKDSTPILFDV
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                                           IVDKFGWCTWDACYLTVDPATIWTGVKEFEDGGVCPKFVIIDDGWQSINFDGDELDKDAE
                                                                                                                                                                                                                                                   PENIVASP-SPYTSIDKSPVSV------GCFVGFDASEPDSRHVVSIGKLKDIRFM
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44.5%;
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Pred. No. 4.5
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Matches 306
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Q40077;
01-NOV-1996 (TrEMBLrel. C
01-NOV-1996 (TrEMBLrel. C
01-DEC-2001 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                                                                                                                                                Seed
                                                                                                                                                                                                       imbibition in barley.";
Submitted (FEB-1992) to the EMBL/GenBank/DDBJ
EMBL; M77475; AA32975 1;
SEQUENCE 757 AA; 82133 MW; EA9E7B771AABBCC
                                                                                                                                                                                                                                                                                                                            Spermatophyta; Magnoliophyta; Triticeae; Hordeum. NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                        Heck G.R., Dorsett
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-HIMALAYA;
                                                                                                                                                                                                                                                                                                                                                                    Hordeum vulgare (Barley).
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                           "Cloning
               135
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LPIVEGPFRTSIQPGDDDFVDVCVESGSSKVVDASFRSMLYLHAGDDPFALVKEAMKIVR
                                                                                                                                                                                                                                                                                                                                                                                                             imbibition
                                                         DIRFMSIFRFKVWWTTHWVGRNGGDLESETQIVILE-----
                                                                                                            DGSDFTVNGHSFLSDVPENIVASPSPYTSIDKSPVSVGGFVGFDASEPDSRHVVSIGKLK
                                          DCREMCLEREKLWWMTQRMGTSGRDVPLETQFILIEVPAAAGNDDGDSSDGDSEPVYLVM
                                                                                             DGR-LAVRGRTVLSGVPDNVTAAHAAGAGLVD----GAFVGATAAEAKSHHVFTFGTLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KCYLNDKEAEFKWEEETGKLSFFVPWV--EESGGISHLSFTF
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yta; Liliopsida;
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Pred. No. 7.8e
28; Mismatches
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Last sequence up
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a; Poales; Poaceae; Pooidea
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Q43408;
Q43408;
O1-NOV-1996 (TrEMBLrel. 01, Created)
O1-NOV-1996 (TrEMBLrel. 02, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Putative imbibition prottein.
Brassica oleracea (Cauliflower).
Brassica oleracea (Cauliflower).
Brassica viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
eurosids II; Brassicales; Brassicaceae; Brassica.
NCBI_TaxID-3712;
                                                                                                       STRAIN-CV. ALPHA BALOMA; TISSUE-ROOT TIPS; Fujikura Y., Karssen C.K.; "Cauliflower cDNA encoding a putative imbibition protein."; Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases. EMBL; X79330; CAA55893.1; -. SEQUENCE 765 AA; 84084 MW; 73398603048E9B58 CRC64;
                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THLGTFRLLEEKTPPGIVDKFGWCTWDAFYLTVHPQGVIEGVRHLVDGGCPPGLVLIDDG
                        MSSPFAIDGSDFTVNGHSFLSDVPENIVASPSPYTSIDKSPVSVGCFVGFDASEPDSRHV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCHMVH----CANDSLWMGNFIHPDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WQQIGSENKDDP----GV-AVQEGAQFASRLTGIRENTKFQSEHNQEET-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KHTQTFHHREKKTVPSFVDWFGWCTWDAFYTDVTADGVKQGLRSLAEGGAPPRFLIIDDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPLLEGQFRTVLQGNDQDELQICIESGDKAVETEQGMNNVYVHAGTNPFDTITQAVKAVE
ITSNISVQNDNLVVQGKTILTKIPDNIILTPVAGAGSDS----
                                                                                                                                                                                                                                                                                                                                                                                                                               ETGEDGNAVVGLRVRGCGRFGAYCSRRPAKCSVDSADVEFTYDSDTGLVTADVPVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WCRETRRNQCFSQYSKRVTSKTNPKDIE-------WHSGENPISIEGVKTFALYLYQ
                                                                  Similarity
                                                     Conservative
                                                                34.9%;
                                                               Score 1473.5;
Pred. No. 3.9
                                                      Mismatches
                                                   .9e-111;
les 253;
                                                                             DB 10; Length
-GAFIGATFKQSKSLHV
                                                     85;
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O94A08.

O1-DEC-2001 (TrEMBLrel. 19, Created)

O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)

O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)

Putative imbibition protein.

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Roside eurosids II; Brassicales; Brassicaceae; Arabidopsis.
SEQUENCE FROM N.A.

Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M.,

Yamada K., Liu S.X., Pham P.K., Bonh J., Banno F., Dale J.M.,

Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L.,

Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L.,

Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones

Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam E
                                                                                                                NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       -DYDDDLSS------VEIGVKGCGEMRVFASKKPRACRIDGEDVGFKYDQ
                                                                                                                                                Rosidae;
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Best Local Similarity 36.6%; Pr
Matches 294; Conservative 157;
 Q9SCM1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy; Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; "Full Length cDNA of gene T8H10.120/AT3g57520 (GI:6706423)."; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY050772; AAK93707.1; -
                                                                         736
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                                                                                                                         AIESIDINHVTDKNPEFFDGEISSASPALSDNRSPTALVSVSVRGCGRFGAYSSQRPLKC
                                                                                                                                                                        -IVYAYRSGEVVRLPKGASIPLTLKVLEYELFHISPL-KEITENISFAPIGLVDMFNSSG
                                                                                                                                                                                    FALYLYQAKKLILSKPSQDLDIALDPFEFELITVSPVTKLIQTSLHFAPIGLVNMLNTSG
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                                                                                                                                                                                                                                     AFNCQGGGWCRETRRNQCFSQYSKRVTSKTNPKDI------EWHSGENPISIEGVKT
                                                                                                                                                                                                                                                                      {\tt DKPGNHNFDLLRKLVLPDGSVLRAKLPGRPTRDCLFADPARDGISLLKIWNMNKFTGIVG}
                                                                                                                                                                                                                                                                                   DSVGKHNFDLLKKLVLPDGSILRSEYYALPTRDCLFEDPLHNGETMLKIWNLNKFTGVIG
                                                                                                                                                                                                                                                                                                                                    PNGTFWLQGCHMVHCAN---DSLWMGNFIHPDWDMFQSTHPCAAFHAASRAISGGPIYVS
                                                                                                                                                                                                                                                                                                                                                                       RVSLTRSYQQALEASIARNFTDNGCISCMCHNTDGLY-SAKQTAIVRASDDFYPRDPAS-
                                                                                                                                                                                                                                                                                                                                                                                              RVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLGTEAISLGRVGDDFWCTDPSGD
                                                                                                                                                                                                                                                                                                                                                                                                                     GNQPDIVMDSLAVHGLGLVNPKKVFNFYNELHSYLASCGIDGVKVDVQNIIETLGAGLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                             MTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGIDGVKIDVIHLLEMLCEDYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TQVSGLKSVVDNAK-QRHNVKQVYAWHALAGYWGGVKPAASGMEHYDSALAYPVQSPGVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----GMKAFIDELKGEFKTVEHVYVWHALCGYWGGLRPQVPGLP--EARVIQPVLSPGLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGWQQIENKEKDENCVVRE-----GAQFATRLVGIKENAKFQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGWQSIGH---DSDPITKEGMNQTVAGEQMPCRLLKFQENYKFRDYVNPKATGPRAGQK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERHMOTFHHREKKKLPSFLDWFGWCTWDAFYTDVTAEGVDEGLKSLSEGGTPPKFLIID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VRTHLGTFRLLEEKTPPGIVDKFGWCTWDAFYLTVHPQGVIEGVRHLVDGGCPPGLVLID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VFLPLLEGQFRAVLQGNEKNEIEICFESGDKAVETSQGTHLVYVHAGTNPFEVIRQSVKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLLPIVEGPFRTSIQPGDDDFVDVCVESGSSKVVDASFRSMLYLHAGDDPFALVKEAMKI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FPIGVLEGLRFMCCFRFKLWWMTQRMGSCGKDIPLETQFMLLESKDEVEGNGDDAPTVYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITSNISVQNDNLVVQGKTILTKIPDNIILTP----VTGNGFVSGSFIGATFEQSKSLHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSSPFAIDGSDFTVNGHSFLSDVPENIVASPSPYTSIDKSPVSVGCFVGFDASEPDSRHV
              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                        HTTHIASVAYNSLFLGEFMQPDWDMFHSLHPTAEYHAAARAVGGCAIYVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34.5%;
                                                                                                                                               -YDDDLSS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1459.5; DB 10; Leng
Pred. No. 5.5e-110;
7; Mismatches 249; Indels
              PRT;
              773
              A
                                                                                                                                               -VEIGVKGCGEMRVFASKKPRAC
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Best Local S
Matches 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ches 294;
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  -IVYAYRSGEVVRLPKGASIPLTLKVLEYELFHISPL-KEITENISFAPIGLVDMFNSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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Benes V., Rechmann S., Borkova D., Ansorge W.,
Mayer K.F.X., Quetier F., Salanoubat M.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBT d
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01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-MAY-2000 (TrEMBLrel. 13, Last annotation
Imbibition protein homolog.
T8H10.120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EU Arabidopsis sequencing project;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ
EMBL; AL133248; CAB66109.1; -
SEQUENCE 773 AA; 85143 MW; 0852F9E67952C8E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FALYLYQAKKLILSKPSQDLDIALDPFEFELITVSPVTKLIQTSLHFAPIGLVNMLNTSG
                                                  VFNCQGAGWCKETKKNQIHDTSPGTLTGSIRADDADLISQVAGEDW-SGDS------
                                                                                                                                                                                 DSVGKHNEDLLKKLVLPDGGSILRSEYYALPTRDCLFEDPLHNGETMLKIWNLNKFTGVIG
                                                                                                                                                                                                                                                                                                                                                                   RVSLTRSYQQALEASIARNFTDNGCISCMCHNTDGLY-SAKQTAIVRASDDFYPRDPAS-
                                                                                                                                                                                                                                                                                                                                                                                                                              RVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLGTEAISLGRVGDDFWCTDPSGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNQPDIVMDSLAVHGLGLVNPKKVFNFYNELHSYLASCGIDGVKVDVQNIIETLGAGLGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DGWQSIGH----DSDPITKEGMNQTVAGEQMPCRLLKFQENYKFRDYVNPKATGPRAGQK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERHMQTFHHREKKKLPSFLDWFGWCTWDAFYTDVTAEGVDEGLKSLSEGGTPPKFLIID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VRTHLGTFRLLEEKTPPGIVDKFGWCTWDAFYLTVHPQGVIEGVRHLVDGGCPPGLVLID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VFLPLLEGQFRAVLQGNEKNEIEICFESGDKAVETSQGTHLVYVHAGTNPFEVIRQSVKA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FLLPIVEGPFRTSIQPGDDDFVDVCVESGSSKVVDASFRSMLYLHAGDDPFALVKEAMKI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       {\tt FPIGVLEGLRFMCCFRFKLWWMTQRMGSCGKDIPLETQFMLLESKDEVEGNGDDAPTVYT}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSIGKLKDIRFMSIFRFKVWWTTHWVGRNGGDLESETQIVILEK-----
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                                                                                                                                                        DKPGNHNFDLLRKLVLPDGSVLRAKLPGRPTRDCLFADPARDGISLLKIWNMNKFTGIVG
                                                                                                                                                                                                                                                                                                                       PNGTFWLQGCHMVHCAN---DSLWMGNFIHPDWDMFQSTHPCAAFHAASRAISGGPIYVS
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                                                                                                                                                                                                                                                                     HTIHIASVAYNSLFLGEFMQPDWDMFHSLHPTAEYHAAARAVGGCAIYVS
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85143 MW; 0852F9E67952C8D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.5%; Score 1458.5; 36.6%; Pred. No. 6.66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     %; Pred. No. 6.6e-110;
157; Mismatches 249; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -GAQFATRLVGIKENAKFQ-
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                                                                                                    -EWHSGENPISIEGVKT
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Query Match
Best Local S
Matches 305
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Q8RX87;
Q0BX887;
Q01-JUN-2002 (TrEMBLrel. 21, Created)
Q1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
AT5q2025Q/F5Q4_140.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidaeurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Arabidopsis cDNA clones.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AY090237; AAL90901.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shinn P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J., Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Sat Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-3702;
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                                                                                                                                                                                                                                                                             CPPGLVLIDDGWQSIGHDSDPITKEGMNQTV-AGEQMP----CRLLKFQENYKFRDYVNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DMTIKPAVRISDGNLIIKNRTILTGVPDNVITT----SASEAGPVE-GVFVGAVFNKEES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AIESIDINHVTDKNPEFFDGEISSASPALSDNRSPTALVSVSVRGCGRFGAYSSQRPLKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AIQSVD-----YDDDLSS-----
  GGLGGRVELTRQFHQALDSSVAKNFPDNGCIACMSHNTDALYCSKQAAVI-RASDDFYPR
                                       EDYGGRVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLGTEAISLGRVGDDFWCT
                                                                                SKGVVENDPTWKTDVMTLQGLGLVSPKKVYKFYNELHSYLADAGVDGVKVDVQCVLETLG
                                                                                                          SPGLQMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGIDGVKIDVIHLLEMLC
                                                                                                                                                                     KKDDPNVGIKNIVKIAKEKHG----LKYVYVWHAITGYWGGVR---PGEEYGSVMKYPNM
                                                                                                                                                                                                                                                     TPPKFVIIDDGWQSVERDA-----TVEAGDEKKESPIFRLTGIKENEKFK----
                                                                                                                                                                                                                                                                                                                                      QTITDAIRTVKLHLNSFRQRHEKKLPGIVDYFGWCTWDAFYQEVTQEGVEAGLKSLAAGG
                                                                                                                                                                                                                                                                                                                                                           VECNOKVYTVFLPLIEGSFRSCLQGNVNDEVELCLESGDVDTKRSSFTHSLYIHAGTDPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----RPYVFLLPIVEGPFRTSIQPGDDDFVDVCVESGSSKVVDASFRSMLYLHAGDDPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DMSSPFAIDGSD--FTVNGHSFLSDVPENIVASPSPYTSIDKSPVSVGCFVGFDASEPDS
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305; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94215 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1446.5; DB 10; Length Pred. No. 7.2e-109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -VEIGVKGCGEMRVFASKKPRAC
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Best Local S
Matches 293
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Q9M4M7;
01-OCT-2000
01-OCT-2000
01-DEC-2001
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293; Conserv
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"Isolation and characterization of cDNAs for mRNAs regulated cold storage of avocado (Persea americana Mill.) fruit."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AJ133148; CAB77245.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-CV. HASS; TISSUE-MESOCARP;
Zamorano J.P., Evans A.D., Dopico B., Lowe A.L.,
Merodio C., Grierson D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Persea americana (Avocado),
Eukaryota; Viridiplantae; Streptophyta;
Spermatophyta; Magnoliophyta; Laurales;
NCBI_TaxID=3435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TERMBLrel. 15, Created)
01-OCT-2000 (TERMBLrel. 15, Last sequence up
01-DEC-2001 (TERMBLrel. 19, Last annotation
Plattive seed imbibition protein.
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                                                                                                                                                                                   KHLYSFQHLEKKKIPSFLDWFGWCTWDAFFTDVTDEGVEEGLKSLSGGGTPPRFLIIDDG
                                                                                                                                                                                                           THLGTFRLLEEKTPPGIVDKFGWCTWDAFYLTVHPQGVIEGVRHLVDGGCPPGLVLIDDG
                                                                                                                                                                                                                                                                                                   LPIVEGPFRTSIQPGDDDFVDVCVESGSSKVVDASFRSMLYLHAGDDPFALVKEAMKIVR 194
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                                           IDELKGEFKTVEHVYVWHALCGYWGGLRPQVPGLP--EARVIQPVLSPGLQMTMEDLAVD
                                                                                        WQQTGSEE---TKDDSNCVVXEGAQFASRLTGIKENDKF-----QKNGKSEHVPGLKLV
                                                                                                                                                                                                                                                                            LPLLEGQFRAVLQGNESNQIEICLESGDCAVRTNQGMYLVYMHAGTNPFQVINQAVKAVE 182
                                                                                                                                                                                                                                                                                                                                                                    LEGLRETCCFRFKLWWMTQRMGMCGKDVPLETQFMLIESKDGAAAIDDDEEEAPTIYTVF
                                                                                                                                                                                                                                                                                                                                                                                              LKDIREMSIFREKVWWTTHWVGRNGGDLESETQIVILEKSDSGRP-------YVFL 134
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VDDAK-QHHNVKFVYVWHALAGYWGGVKPPAAGMEHYDTALAYPVQSPGVMGNQPDIVMD
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SEQUENCE FROM N.A.
Shinn P.P., Buehler E.E., D
Walker M.M., Altafi H.H., A
Gonzalez A.A., Hansen N.N.F
Lenz C.C., Li J.J., Liu S.S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9LFZ7;
Q9LFZ7;
01-OCT-2000
01-OCT-2000
01-JUN-2002
F20N2 14.
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

Khan S., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Kim C., Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J. Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A., Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Roside

eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID-3702;
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Ecker J.R.;
                                                                                                                                                   Submitted
                                                                                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                               Submitted
                                                                                                                                                                                                                                                                                                                                                                                          "Genomic sequence for
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EMBL; AC002328: AAR795041; -.

InterPro: IPR004798; Cax.

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Search completed: April 4, 2003, 11:12:35 Job time : 48 secs



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ALIGNMENTS

RESULT

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A;Recession: C85025
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-807 <570>
A;Residues: 1-807 <570> R; anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Nature 402, 769-777, 1999 hypothetical protein AT4901970 [imported] - Arabidopsis thaliana (Syspecies: Arabidopsis thaliana (mouse-ear cress) C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001 C:Accession: C85025 A; Gene: AT4g01970 A; Cross-references: A; Map position: Best Loc Matches Genetics: Query Match 391 351 331 291 171 151 114 SLFRFKMWWSTAWIGKSGSDLQAETQWVMLKIPEIDS---YVAIIPTIEGAFRASLTPGE 170 93 54 44 Match 43.9%;
Local Similarity 44.5%;
les 366; Conservative 146 ,_ 1 MAPSFKNGGSNVVSFDGLNDM--SSPFAI-------DGSDFTVNGHSFLSDV 43 HALCGYWGGLRPQVPGLPEARVIQPVLSPGLQMTMEDLAVDKIVLHKVGLVPPEKAEEMY NQTVAGEQMPCRLLKFQENYKFRDYVNPKATGPRAGQKGMKAFIDELKGEFKTVEHVYVW IVDKFGWCTWDAFYLTVHPQGVIEGVRHLVDGGCPPGLVLIDDGWQSIGHDSDPITKEGM KGNVLICAESGSTKVKESSFKSIAYIHICDNPYNLMKEAFSALRVHMNTFKLLEEKKLPK SIFRFKVWWTTHWVGRNGGDLESETQIVILE--KSDSGRPYVFLLFIVEGFFRTSIQPGD 150 PQNVTFTPFSSHSISTDAPLPILLRVQANAHKGGFLGFTKESPSDRLTNSLGRFEDREFL 113 EGLHAHLEKVGIDGVKIDVIHLLEMLCEDYGGRVDLAKAYYKAMTKSINKHFKGNGVIAS HALCGAWNGVRPETMMDLKAKVAPFELSPSLGATMADLAVDKVVEAGIGLVHPSKAHEFY IVDKFGWCTWDACYLTVDPATIWTGVKEFEDGGVCPKFVTIDDGWQSINFDGDELDKDAE PENIVASP-SPYTSIDKSPVSV-------GCFVGFDASEPDSRHVVSIGKLKDIRFM MAPLHE----SLSSINDVIESKPLFVPITKPILQPNSFNLSEGSLCAKDSTPILFDV NLVLGGEQMTARLTSFKECKKFRNYKEESLGSDDVSGSGMAAFTKDLRLRFKSLDDIYVW GB:NC_001268; NID:g7268581; PIDN:CAB80690.1; GSPDB:GN00140 146; Score 1853.5; DB 2; Pred. No. 1.5e-138; 6; Mismatches 257; Indels Length 807; 53; Gaps 390 330 290 270 210 92 53 350 230 14; g

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RESULT 2
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$197 protein - barley
$1978 c; Species: Hordeum vulgare (barley)
$C; Species: Hordeum vulgare (barley)
$C; Date: 17-Apr-1993 #sequence_revision 17
$C; Accession: $27762
$R; Heck, G.R.; Dorsett, C.; Ho, T.H.
$ubmitted to the EMBL Data Library, Febru.
$A; Description: Cloning and characterizati.
$A; Percence number: $27762
$A; Accession: $27762
$A; Molecule type: DNA
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                                            FIDELKGEFKTVEHVYVWHALCGYWGGLRPQVPGLP--EARVIQPVLSPGLQMTMEDLAV
                                                                                                                                  WQSIGHDS--DPITKEGMNQTVAGEQMPCRLLKFQENYKFRDYVNPKATGPRAGQKGMKA 312
                                                                                                                                                                                 KHTQTFHHREKKTVPSFVDWFGWCTWDAFYTDVTADGVKQGLRSLAEGGAPPRFLIIDDG
                                                                                                                                                                                                                             THLGTFRLLEEKTPPGIVDKFGWCTWDAFYLTVHPQGVIEGVRHLVDGGCPPGLVLIDDG
                                                                                                                                                                                                                                                                       LPLLEGQFRTVLQGNDQDELQICIESGDKAVETEQGMNNVYVHAGTNPFDTITQAVKAVE
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                                                                                          WQQIGSENKDDP----GV-AVQEGAQFASRLTGIRENTKFQSEHNQEET-----PGLKR
                                                                                                                                                                                                                                                                                                                                                                DCRFMCLFRFKLWWMTQRMGTSGRDVPLETQFILIEVPAAAGNDDGDSSDGDSEPVYLVM
                                                                                                                                                                                                                                                                                                                                                                                                          DIRFMSIFRFKVWWTTHWVGRNGGDLESETQIVILE-------KSDSGRPYVFL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DGR-LAVRGRTVLSGVPDNVTAAHAAGAGLVD-----GAFVGATAAEAKSHHVFTFGTLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGSDFTVNGHSFLSDVPENIVASPSPYTSIDKSPVSVGCFVGFDASEPDSRHVVSIGKLK 87
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Library, February 1992
characterization of a gene,
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probable imbibition protein - wild cabbage C;Species: Brassica oleracea (wild cabbage) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 C;Accession: S45033 R;Fujikura, Y; Karssen, C.K. submitted to the EMBL Data Library, May 1994 A;Description: Cauliflower cDNA encoding a putative A;Reference number: S45033 A;Accession: S45033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-765 < FUJ>
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SVVDNAK-QRHNVKQVYAWHALAGYWGGVKPRASGMEHYDSALAYPVQSPGVLGNQPDIV
                                                AFIDELKGEFKTVEHVYVWHALCGYWGGLRPQVPGLP--EARVIQPVLSPGLQMTMEDLA
                                                                                                      WQQIENKEKDSNCLVQE-----
                                                                                                                                                   WQSIGH----DSDPITKEGMNQTVAGEQMPCRLLKFQENYKFRDYVNPKATGPRAGQKGMK 311
                                                                                                                                                                                                         ROMOTFHHREKKKLPSFVDWFGWCTWDAFYTDVTAEGVDEGLRSLSEGGTPPRFLIIDDG
                                                                                                                                                                                                                                                         \tt THLGTFRLLEEKTPPGIVDKFGWCTWDAFYLTVHPQGVIEGVRHLVDGGCPPGLVLIDDG
                                                                                                                                                                                                                                                                                                               LPLLEGQFRAVLQGNEKNEIEICLESGDKAVGTSQGTHLVYVHAGTNPFEVITQSVKAAE
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N;Alternate names: protein T8H10.120
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
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A; Residues: 1-773 <BEN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Benes, V.; Rechmann, S.; Borkova, D.; Ansorge, W.; Mewes, H.W.; Lemcke, K.; Mayer, K. submitted to the Protein Sequence Database, January 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: T46188
R; Benes, V.; Rechman
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A;Introns: 64/2: 146/1; 176/2; 192/3; 223/2: 259/2; 300/2; 484/3; 507/2;
                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: EMBL: AL133248
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Best Local
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                              VRTHLGTFRLLEEKTPPGIVDKFGWCTWDAFYLTVHPQGVIEGVRHLVDGGCPPGLVLID 252
                                                                                     FLLPIVEGPFRTSIQPGDDDFVDVCVESGSSKVVDASFRSMLYLHAGDDPFALVKEAMKI 192
                                                                                                                                                          VSIGKLKDIRFMSIFRFKVWWTTHWVGRNGGDLESETQIVILEK------SDSGRPYV 13:
                                                                                                                                                                                                                                           MSSPFAIDGSDFTVNGHSFLSDVPENIVASPSPYTSIDKSPVSVGCFVGFDASEPDSRHV 80
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                                                                   VFLPLLEGQFRAVLQGNEKNEIEICFESGDKAVETSQGTHLVYVHAGTNPFEVIRQSVKA 177
                                                                                                                                      FPIGVLEGLRFMCCFRFKLWWMTQRMGSCGKDIPLETQFMLLESKDEVEGNGDDAPTVYT 117
                                                                                                                                                                                                       ITSNISVQNDNLVVQGKTILTKIPDNIILTP----VTGNGFVSGSFIGATFEQSKSLHV 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NTVTDEKPELSSSSVVSENRSPTALISLGVRGCGRFGAYSSQRPLRCAVDGTETEFNYDA 740
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VERHMOTFHHREKKKLPSFLDWFGWCTWDAFYTDVTAEGVDEGLKSLSEGGTPPKFLIID
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                                                                                                                                                                                                                                                                                294;
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imilarity 36.68;
Conservative 157
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                                                                                                                                                                                                                                                                            %; Score 1458.5;
%; Pred. No. 3.1e-
157; Mismatches
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26 AIDGSDFTVNGHSFLSDVPENIVASP-SPYTSIDKSPVSVGCFVGFDASEPDSRHVVSIG 84

Query Match Matches

Local Similarity nes 259; Conserv

Conservative 135;

27.0%;

Score 1140; DB 2; Pred. No. 1.1e-81; 35; Mismatches 208

208;

Gaps

20;

Length 1170; Indels 176;

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protein F20N2.14 [imported] - Arabidopsis thaliana
C;Specles: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: C96599
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; A
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewa
ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; K
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Mar
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, S.X.; Luros, J.S.; Maiti, R.; Mar
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Ta
A;Taltle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Salzens need impary
A; Map position:
                              A; Gene: F20N2.14
                                                       C; Genetics:
                                                                                                       A; Molecule type: DNA
A; Residues: 1-1170 <STO>
                                                                                                                                                            A; Status: preliminary
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                                                                           A;Cross-references: GB:AE005173; NID:g8778496; PIDN:AAF79504.1; GSPDB:GN00141
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A;Cross-references: EMBL:X95875; NID:g1212811
A;Experimental source: germinating seed
C:Genetics:
A;Gene: sip
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T09530

C; Species: Cicer arietinum (chickpea, garbanzo)
C; Species: Cicer arietinum (chickpea, garbanzo)
C; Date: 16-U1-1999 #sequence_revision 16-U1-1999 #text_change 20-Jun-2000
C; Accession: T09530
C; Accession: T09530
R; Cervantes, E.
                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-357 <CER>
                                                                                                                                                                                      submitted to the EMBL Data Library, February 1996 A; Reference number: Z16718 A; Accession: T09530
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Matches 127; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVKVDVQNILETLGAGHGGRVKLAKKYHQALEASISRNEPDNGTISCMSHNTDGLY-SAK 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVKIDVIHLLEMLCEDYGGRVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLCTE 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLP--EARVIQPVLSPGLQMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGID 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGETMLKIWNLNKFTGVIGAFNCQGGGWCRETRRNQCFSQYSKRVTSKTNPKDIEWHSGE 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KTAVIRASDDFWPRDPAS------HTIHIASVAYNTLFLGEFMQPDWDMFHSLHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GMEHYESKVAYPVSSPGVMSSENCGCLESITKNGLGLVNPEKVFSFYNDLHSYLASVGVD 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----KDGKEGHRVDDPSLSLGHVITDIKSN-NSLKYVYVWHAITGYWGGVKPGVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YVNPKATGPRAGQKGMKA------FIDELKGEFKTVEHVYVWHALCGYWGGLRPQVP 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KSQLKTSLCPNFFRM-----PDMLNWFGWCTWDAFYTNVTAKDVKQGLESNCDLTKPAL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RTHLGT-----FRLLEEKTPPGIVDKFGWCTWDAFYLTVHPQGVIEGVRHLVD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ILEGDFRAVLQGNEANELEICLESGDPTVDQFEGSHLVFVAAGSDPFDVITKAVKYVMFL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IVEGPFRTSIQPGDDDFVDVCVESGSSKVVDASFRSMLYLHAGDDPFALVKEAMKIV--- 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLEDLRFMCVFRFKLWWMTQRMGTNGKEIPCETQFLIVEANQGSDLGGRDQSSSYVVFLP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVTDSDLVVLGHRVLHGVPENVLVTPASGNALID-----GAFIGVTSDQTGSHRVFSLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----GGCPPGLVLIDDGWQSIGHDSDPITKEGMNQTVAGEQMPCRLLKFQENYKFRD 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLKDIRFMSIFRFKVWWTTHWVGRNGGDLESETQIVILEKS-----DSGRPYVFLLP 136
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.6%; Score 490.5; DB 2; 32.5%; Pred. No. 6.2e-31; tive 55; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----TSLPVTLMPREYEVFTVVPVKEFSDGS-KFAPV 599
                                   Length 357;
   Indels
   55;
 Gaps
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DKIVLHKVGLV 381	QY 322 KTVEHVYVWHALCGYWGGLRPQVPGLPEARVIQPVLSPGLQMTMEDLAVDKIVLHKVG	
GHVITDIKSN- 215	Db 168 NADSAA-NFANRLTHIKEKHKFQKDGKEGHRVDDPALSLGHVITDIKSN-	
FIDELKGEF 321	DYVNPKATGP	
MDETSVEF 167	Db 114 CTWDAFYRKVLRDCDLTKPAIILCSLKAGVVTPKFVIIDDGWQSVGMDETSVEF	
HDSDPITKEGM 270	Qy 218 CTWDAFYLTVHPQGVIEGVRHLVDGGCPPGLVLIDDGWQSIGF	
FMPDMLNWFGW 113	Db 87 LESGKLTQLARFELKLF	
TPPGIVDKFGW 217	Qy 158 VESGSSKVVDASFRSMLYLHAGDDPFALVKEAMKIVRTHLGTERLLEEKTPPGIVDKFGW	
QGNEANELEIC 86	Db 27 MGTNGKEIPCETQFLIVEANKGSGLGGGDESSSYVVFLPILEGDERAVFQGNEANELEIC	
QPGDDDFVDVC 157	Oy 106 VGRNGGDLESETQIVILEKSDSGRPYVFLLPIVEGPFRTSIQPGDDDFVDVC	
ls 173; Gaps 18	9; 12;	
th 371;	1.5;	
5/1; 333/2; 349/2	A;Introns: 5/2; 25/3; 103/3; 126/1; 174/2; 240/1; 284/1; 295 A;Note: A_IG002N01.5	
	C; Genetics: A: Map position: 4	
56	91126; PID:g21911	
	A; Molecule type: DNA A; Residues: 1-371 <sch></sch>	
	A; Status: translated from GB/EMBL/DDBJ	
	A;Reference number: 214407	
	submitted to the EMBL Data Library, June 1997 A; Description: The sequence of A, thaliana IG002N01.	
	C;Accession: T01717 R;Scheet, P.; Maggi, L.	
_change 24-Mar-1999	text	
	T01717 T01717 hypothetical protein A_IG002N01.5 - Arabidopsis thaliana	
	PROTE 7	
	Db 326 RAIGGCQFMSVISQATTILIFLRSLVLADGS 356	
	QY 529 RAISGGPIYVSDSVGKHNFDLLKKLVLPDGS 559	
LHPAAEYHAAA 325	Db 277 DDFYPHDPASHTIHISSVAYNSLFLGEFMQPDWDMFHSLHPAAEYHAAA	
THPCAAFHAAS 528	QY 472 DDFWCTDPSGDPNGTFWLQGCHMVHCANDSLWMGNFIHPDWDMFQST	
SAKQTAIVRAS 276	Db 218 LLRPLVLDTVVESRLHAAIIMRLRLPLLVTLLNNGCIACMCHNTDGLY-SAKQTAIVRAS	
GTEAISLGRVG 471	OY 412 LLEMLCEDYGGRVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLGTEAISLGRVG	
GVDGVKVDVQT 217	Db 161 ATSAVTRSTWNQPDIVMDSLAVHGLRLVHPRGETSTNE-THAYLASCGVDGVKVDVQT	
GIDGVKIDVIH 411	QY 352 VIQPVLSPGLQMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGIDGVKIDVIH	
ATGMEHYDTAL 160	Db 102 NSKNKNGQNDEQIPGLKHLVDGVK-KHHNVKDVYVWHALAGYWGGVKPAATGMEHYDTAL	
VPGLPEAR 351	Oy 300 ATGPRAGOKGMKAFIDELKGEFKTVEHVYVWHALCGYWGGLRPOV	
QLLLGDWIRDA 101	Db 63 RFLIMTMYGNRLKVKQSKGSGCVVQEGAQLLLGDWIRDA	
KFRDYVNPK 299	.DDGWQSIGHDSDPITKEGMN	
IKSLSEGGTPP 62	Db 3 QQAVKAVEKHMQTFHHREKKRVPSFLDWFGWCTWDAFYTDVTAEGVEEGLKSLSEGGTPP	
VRHLVDGGCPP 246	Qy 187 KEAMKIVRTHLGTFRLLEEKTPPGIVDKFGWCTWDAFYLTVHPQGVIEGVRHLVDGGCPP	

Db 319ÓELMKSLNVNGYFTNFLNSYVÞSPNLEÐAIGFYKAFDGNILR-DFDLVKVÐ 368 Qy 409VIHLLEMLCEÐYGG-RVDLAKAYYK-AMTKSINKHFKGNGVIASMEHCNDFM 458	Qy 353 IQPVLSPGLQMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGIDGVKID 408	Qy 293 RDYVNPKATGPRAGQKGMKAFIDELKGEFKTVEHVYVWHALCGYWGGLRPQVPGLPEARV 352 Db 286PNGFKNTVRAIKSLGVKYVGLWHAINAHWGGMS 318	Oy 235 GVRHLVDGGCPPGLVLIDDGWQSIGHDSDPITKEGMNQTVAGEQMPCRLLKFQENYKF 292	Qy 178 AGDDPFALVKEAMKIVRTHLGTFRLLEEK-TPPGIVDKFGWCTWDAFYLTVHPQGVIE 234	Qy 119 IVILEKSDSGRPYVFLLPIVEGPFRTSIQPGDDDFVDVCVESGSSKVVDASFRS-MLYLH 177 :::::::::::::::::::::::::::::::::::	Oy 62 VSVGCFVGFDASEPDSRHVVSIGKLKDIRFMSIFRFKVWWTTHWVGRNGGDLESETQ 118	Qy 28 DGSDFTVNGHSFLSDVPENIVASPSPYTSIDKSP 61	Query Match 8.6%; Score 365; DB 2; Length 649; Best Local Similarity 24.0%; Pred. No. 1.4e-20; Matches 156; Conservative 101; Mismatches 218; Indels 174; Gaps 32;	A;Cross·references: GB:AE006641; NID:gl3816550; PIDN:AAK43227.1; GSPDB:GN00155 C;Genetics: A;Gene: SSO3127	an der OOST, J. plete genome.	-May-2001 #t Zivanovic, Medina, N.;	RESULT 8 190496 hypothetical protein SSO3127 (imported) - Sulfolobus solfataricus	Qy 555 LPDGSIL 561 Db 365 LQDGSIL 371	Qy 500 -DSLWMGNPIHPDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNEDLLKKLV 554 :: :: :	Qy 442 FKGNGVIASMEHCNDFMFLGTEAISLGRVGDDFWCTDPSGDPNGTFWLQGCHMVHCAN 499	Qy 382 PPEKAEEMYEGLHAHLEKVGIDGVKIDVIHLLEMLCEDYGGRVDLAKAYYKAMTKSINKH 441	216 NSLKYVYVWHAITGYWGGVKPSVSGIMSNENCGC
Db 403 PIFGDDGMKNLAVPTLIVAGSKDIFAPPVPEQIIPFSLIEGVNKYLLLVO-NGTHL 457 Qy 408 DVIHLLEMLCED-YGGRVDLAKAYYKAM 434 : :	Qy 359 PGLQMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGIDGVKI 407	Qy 337IQPVLS 358 Operation of the content	Qy 294 D-YVNPKATGPRAGQKGMKAFIDELKGEFKTVEHVYVWHALCGY 336 : : : : : :	Qy 240 VDGGCPPG-LVLIDDGWQSIGHDSDPITKEGMNQTVAGEQMP-CRLLKFQENYKFR 293	QY 186 VKEAMKIVRTHLGTFRLLEEKTPPGIVDKFGWCTWDAFYLTV-HPQG-VIEGVRHL 239	Qy 130 PYVELLPIVEGPFRTSIQ-PGDDDEVDVCVESGSSKVVDASFRSMLYLHAGDDDFAL 185	Qy 77 SRHVVSIGKLKDIRFMSIFRFKVWWTTHWVGRNGGDLESETQIVILEKSDSGR 129 :: :	Qy 21 MSSPFAIDGSDFTVNGHSFLSDVPENIVASPSPYTSIDKSPVSVGGFVGFDASEPD 76	Ouery Match 2.9%; Score 121.5; DB 2; Length 538; Best Local Similarity 21.5%; Pred. No. 0.22; Matches 109; Conservative 79; Mismatches 185; Indels 135; Gaps 29;	A;Reference number: \$74432; MUID:97061201; PMID:8905231 A;Accession: \$76481 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-538 «KAN> A;Residues: 1-538 «KAN> A;Residues: 1-538 «KAN> A;Residues: 1-538 «KAN> A;Residues: the nucleotide sequence was submitted to the EMBL Data Library, June 1996 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996	R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas DNA Res. 3, 109-136, 1996 A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys.	C;Species: Synechocystis sp. C;Species: Synechocystis sp. C;Acriety: PCC 6803 C;Date: Synechocystis sp. C;Accession: S76481 C:Accession: S76481	RESULT 9 \$76481 hypothetical protein - Synechocystis sp. (strain PCC 6803)	Qy 573 CLFEDPLHNGETMLKTWNLNKFTGVIGAFNCQGGGWCRETRRNQCFSQY 621 : : :	Qy 517 STHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALPTRD 572	QY 459 FLGTEAISLGRVGDDFWCTDPSGDPNGTFWLQGCHMVHCANDSLWMGNEIHPDWDMFQ 516	Db 369 NQWVIHAIYDSFPIGLASRNIQIALQYSVGKDVINCMSMNPENYCN-YF 416

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A;Cross-references: EMBL:ALO31324; PIDN:CAA20445.1;
A;Experimental source: strain 972h-; cosmid c1672
C;Genetics:
C;Gene: SPDB:SPCC1672.07
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C;Date: 03-Dec-1999 #sequence_revision
C;Accession: T41051
R;Hilbert, H.; Duesterhoeft, A.; Wood,
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A; Residues: 1-902 <HIL>
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A; Accession: T41051
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     RIDGEDVGFKYDQDQMVVVQVPWPIDSSSGGISVIE
                                                                                                       DDFGIRIVDVQTRKIVRELWGHSNRLTSFDFSDTGRWLVTASLDGTIRTWDLPTGHLIDS
                                                                                                                                                                        KPVTAVMLDNVNRILVTASLDGILKFWDFNKGNLIDSLDVGSSITHAIYQHSSDLVAVAC
                                                                                                                                                                                                                                            QHVLPTSDGTSVRSVCVSCCGNFGLIGSSKGVVDVYNMQSG-
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                                        ISTPSVCTSLTFAPTG
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                                                                                                                                                                                                                                                                                                           QGSVISKAKKLNVRPEELKLPEITALSSSNTREKYWDNVLTAHKNDSSARTWNWKSKTLG
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                                                                                                                                                                                                                                                                                                                                                                            RSRNGHYEPPSFVKFYGKSVHFLISAATDRSLRAVS---LY-QDS---
                                                                                                                                                                                                                                                                                                                                                                                                              ----GNFIHPDWDMF--QSTH--PCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLP 556
                                                                                                                                                                                                                                                                                                                                                                                                                                               DLSFWDLSKRRIQNVTYNAHFGSLPKIQFLNGQPILVTAGPDNSLKEWIFDSMDGAPRIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DVLAVGTISGRI----VIFNLKNGSILMEFKQDGQVLSCSFRTD----GTPILASSNPIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMLC-EDYGGRVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLGTEAI-SLGRVG 471
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139; Conser
                                                                      -TSLHFAPIGLVNMLNTSGAIQSVDYDDDLSSVEIGVKGCGEMRVFASKKPRAC
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August 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -WLQGCHMVHCA - - NDSL - -WM - - -
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                                                                                                                                                                                                                                                                          -GVIGAFNCQGGGWCRETRRNQCFSQYS---
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C;Genetics:
A;Gene: SGD
                                                  A; Molecule type: DNA
A; Residues: 1-632 <DIE>
                                                                                    A; Reference number: A; Accession: S69702
                                                                                                                   submitted to the EMBL Data Library, A:Description: The sequence of S. co
                                                                                                                                                                    hypothetical protein YDR419w - yeast (Saccharomyces cerevisiae) C;Species: Saccharomyces cerevisiae C;Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change C;Accession: S69702
                                                                                                                                                                                                                                         RESULT
S69702
                                    A; Cross-references:
                                                                                                                                                      R; Dietrich, F.S.
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C;Superfamily: polypeptide N-acetylgalactosaminyltransferase
C;Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biol. Chem. 273, 8268-8277, 1998
A; Title: cDNA cloning and expression of a A; Reference number: Z22126; MUID:98192620;
                                                                                                                                                                                                                                                                                                                                         20
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A; Residues: 1-623 < HAG>
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J. Biol. Chem. 273, 8268-8277, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable polypeptide N-acetylgalactosaminyltransferase (EC C;Species: Caenorhabditis elegans
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                                    EMBL: U33007; NID: g927685; PIDN: AAB64856.1; PID: g927690; MIPS: YDR4
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21.7%;
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                                                                                                                     Cerevisiae la
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and

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A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: I64118
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-730 <TIGR>
                                                                                                                                                                                                                                                                                                        R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weldman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: I64118
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                                        83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FALYLYQAKKLIL--SKPSQDLDIALDPFEFELITVSPVTKLIQTSLHFAPIGL 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --PEKAEEMYEGLHAHLEKVGIDGVKIDVIHL---LEMLCEDYGGRVDLAKAYYKAMTKS 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EHVYVWHALCGYWGGLRPQVPGLPEARVIQPVLSPGLQMTMEDLAVDKIVLHKVGLVP-- 382
  VNFRLWAPNARRVSIVGDF---
                                      VGFDASEPDSRHVVSIGKLKDIRFMSIFRFKVWWTTHWVGRNGG---DLESETQIVILEK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----FOSHELLKVGIKFVTDLDI-----KGKNKSYYPLTKLSMTITNFDIIDL 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -------WCRE-TRRNQCFSQ-YSKRVTSKT-----NPKDIEWHSGENPISIEGVKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDY----DRSTSNIDPLKTADLAEKLFKLSRGRYGLPLSSRPVVKSMMSNKNLRGKSCNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ITSFWTLGGVL-----GKELIDVLD---LPHENSIKHIRETWPDNAGQLKEFLDAKVKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IVDCISWLEVFCAELTSRIQDLEQEYNKIVIPRTVSISLKTKSYEVYRKSGPVAYKGIN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IREAFIGGNY-----DINSHLPLIPEKIKSLKFEGDVF---NPEGRDLITDWDDVILALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INKHFKGNGVIASMEHCNDFMFLGTEAI-SLGRVGDDFWCTDPSGDPNGTFW-----
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                                                                                                  Similarity
                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.78;
                                                                           2.5%; Score 105; DB 1;
17.5%; Pred. No. 7.3;
ative 75; Mismatches 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -LQGCHMVHCANDSLWMGNFIHPDW-----DMFQSTHPCAAEH
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Pred. No. 1.2;
----NYWDGRRHPMRFHSKSGVWELFLPK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                 203;
                                                                                                                    Length 730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 169;
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T19997
                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, A; Reference number: Z19209
A; Accession: T19997
                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein C47D12.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T19997
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В
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                                                                                                                                                        A; Map position: 2
A; Introns: 46/3; 308/3;
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A; Residues: 1-3944 <WIL>
A; Cross-references: EMBL: Z69902; PIDN: CAA93765.1; GSPDB: GN00020; CESP: C47D12.1
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                                                                                                                                                                                                     A; Gene: CESP:C47D12.1
                                                                                                                                                                                                                                              A; Experimental source: clone C47D12
                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; translated from GB/EMBL/DDB.
                                                                               Matches
                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                           Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             630
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                                      80
                                                                               Local Similarity es 136; Conser
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VVSYGHVKILQAMNLVR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VKNFLSSNALYWLERFGVDGIRVDAVASMIYRDYSRAEGEWIPNQYGGRENLEAIEFLKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NYKFRDYVNPKATGPRAGOKGMKAFIDELKGEFKTVEHVYVWHALCGYWGGLRPQVPGLP 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGDDPFALVKEAMKIVRTHLGTFRLLEEKTPPGIVDKFGWCTWDAFYLTVHPQGVIEGVR 237
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                                    VVSIGKLKDIRFMSIFRFKVWWTTHWVGRNGGDLESETQIVILEKSDSGRPYVFLLPIVE 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HL------VDGGCPPGLVLIDDGWQSIGHDSDPITKEGMNQTVAGEQMPCRLLKFQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QGNQP-----ISIYEVHLGSWR-----RNLENNF-WLDYDQIADELIPYVKEMGFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLLFMGNEFAQGREWNYEESLDWFLLDENIGGGWHKGVLKLVKDLNQIYQKNRPLFELDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------NQCFSQYSKRVTSKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----SENFVLPLS---HDEVVHGKYSLLGKMPGDTWQKFANLRAYYGYMWGYPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MTKSINKHEKGNGVIASMEHCNDFMFLGTEAISLGRVGDDFWCTDPSGDPNGTFWLQGCH
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                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----RAHEAGINVILDWVPGHFPSDTH-----
                                                                                                                                                             408/2; 449/3; 820/3; 946/3; 1069/1; 1634/3;
                                                                             2.4%; Score 103; DB 2;
18.5%; Pred. No. 1.4e+02;
tive 90; Mismatches 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----AYMKLDPIYRQYHHNKMTFGMVYQY
                                                                                                                                                                                                                                                                                                                                                                                          March 1996
----EIEESTDIRI---
                                                                                                                 Length 3944;
                                                                                                                                                             1737/2; 2009/2;
                                                                             Gaps
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2957
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Que Bes Mat	RESULT G90524 hypothe C; Speci C; Dacces R; Chamb Nucleic A; Title A; Refer A; Refer A; Refer A; Statu A; Molec A; Cross A; Cross C; Cross	Оy	ОУ	Qу	Оy	Db Qy	Qy	Qy	Оy	Оу Дъ	Qy Db	Qy	Qу
Query Matc Best Local Matches	fi iii suusse t	701 3470	652 3411	609 3363	563 3305	503 3280	448 3240	415 3180	375 3121	315	259 3021	200 2984	140 2958
82 5	RESULT 15 G90524 hypothetical protein MYPU_1030 [imported] - My C;Species: Mycoplasma pulmonis C;Date: 24-May-2001 #sequence_revision 24-May- C;Accession: G90524 R;Chambaud, I; Heillg, R; Ferris, S; Barbe, Nucleic Acids Res. 29, 2145-2153, 2001 Nucleic Acids Res. 29, 2145-2153, 2001 A;Title: The complete genome sequence of the m A;Reference number: A99512; MUID:21267165; PMI A;Accession: G90524 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-544 <kur- a;cross-references:="" a;experimental="" a;gene:="" alpha-amylas<="" alpha-glucosidase;="" c;genetics:="" c;superfamily:="" ctip="" gb:al445566;="" mypu_1030="" pid:g14089516="" source:="" strain="" td="" uab=""><td>GLVNMLNTSGAIQSVD : : : : NMTNMMVSQLDIHAVD</td><td>ALYLYQAKKLILSKPSQDLDIALDPFEBELITVSPVTKLIQTSLHFA </td><td>RHLRHA</td><td>SEY</td><td>WMGNFI</td><td>IASMEH KKQLH</td><td>FFSTTV</td><td>KDQVA</td><td>DELKGE :: NKLAG-</td><td>GHDSDE : GLN</td><td>FRLLEE</td><td>GPFRTSIQPGDDDFVDVCVESGSSKVVDASFRSMLYLHAGDDPFALVKEAMKIVRTHLGT</td></kur->	GLVNMLNTSGAIQSVD : : : : NMTNMMVSQLDIHAVD	ALYLYQAKKLILSKPSQDLDIALDPFEBELITVSPVTKLIQTSLHFA	RHLRHA	SEY	WMGNFI	IASMEH KKQLH	FFSTTV	KDQVA	DELKGE :: NKLAG-	GHDSDE : GLN	FRLLEE	GPFRTSIQPGDDDFVDVCVESGSSKVVDASFRSMLYLHAGDDPFALVKEAMKIVRTHLGT
imilarity ; Conserva	protein MYPU_10 YCOPLASMA PULMON G90524 I; Heilig R; complete genome complete 99512; 1 G90524 liminary /Pe: DNA L:54 <kur> L:544 <kur> 1.544 <kur> 1.130 1.130 1.130 1.130 1.130 1.130 1.130 1.130 1.30 1</kur></kur></kur>	NTSGA:)	-CRETI	YAI	HPDWDI	IASMEH-CNDFMFLGTEAISLGRVGDDFW	MLCEDYG- : ::: TVCKETGN	LLYHR	EFKTVEI : -LTAIPI	GHDSDPITKEGMNQTV- : :: CLNVAATG-NQSIV	EEKTPPGIVDKFGWCTWDAFYLTVHP 	SIQPGD
rt	ma pulmonis #sequence_re #sequence_re lig, R; Ferr 29, 2145-213; MUID A99512; MUID A99512; MUID Ce: Strain UA		FLEIRN	CRETRRNQCFS- : : CLKDQMFKDFSE	PTRDC	MFQSTH : AAH	MFLGTE	GRV } NNFGRQ	LHKV NIHSV	HVYVWH ; MMDAQD	VISON-	IVDKFG SDDMGF	DDFVDV
2.4%; 20.7%; ive 4	PU_1030 [importulemonis squence_revision R: Ferris, S. 2145-2153, 2001 senome sequence 5512; MUID:21267	716 3485	AKKLII : : :	S SEQMDA	LFEDPI : FADDPI	PCAAFI PLQVFY	AISLGR	GRVDLAKAYYKA- : NFGRQALACYFIAAR	GLVPPI - LDQAI	ALCGYV : KVCTY	ΡI	WCTWD!	CVESG: : : LLEAP:
Score Pred 18; M	[imported] evision 24 ris, S.; B 3, 2001 quence of D:21267165 D:21267165		SKPSQ:	TENEM	HNGETI	AASRA HIREA	WGDDF	YKA	LHKVGLVPPEKAEEMYEG : : :HSV-LDQAENADYTFSAAS	VGGLRP KTLRD	EQMPCR \QAQLA	AFYLTV : : DWRNQI	VCVESGSSKVVDASFR:
Score 102.5; Pred. No. 7.3; 8; Mismatches	330 [imported] - Mycoplas is is e_revision 24-May-2001 # Ferris, S.; Barbe, V.; S 2153, 2001 sequence of the murine MUID:21267165; PMID:1135 MUID:21267165; PMID:1135		AKKLILSKPSQDLDIALDPFEFELITVSPVTKLIQTSLHFAPI		SEYYALPTRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGW	WMGNPIHPDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILR	2 :	MLCEDYGGRVDLAKAYYKA	LHKVGLVPPEKAEEMYEGLHAHLEKVGIDGVKIDVIHLLE-	DELKGEFKTVEHVYVWHALCGYWGGLRPQVPGLPEARVIOPVLSPGLQMTMEDLAVDKIV ::	PITKEGMNQTVAGEQMPCRLLKFQENYKFRDYVNPKATGPRAGQKGMKAFI	FRLLEEKTPPGIVDKFGWCTWDAFYLTVHPQGVIBGVRHLVDGGCPPGLVLID-DGWQSNRTPTTSDDMGFVSTWYDWRNQIHGMMLQRFEYWDK	ASFRSM ALM
DB 1	e ; D:		DPFEFE IMFEKE	TSKTNF	WN : KYRPTE	YVSDSV	TDPSGL TDVRYK	RKPIAK	LHP LHP	EARVIC : DERVKN	NYKFRE † ; NLGFHN	EGVRHL	LYLHAGDD GD-
2;	ma tex res 308		LITVS	KDIEWHS : LRWR-	LNKFT	GKHNF	PNGTF	TLWLS	HLEKV : ISVTTT	PVLSP : ELLCE	YVNPK	VDGGC	HDDPFA
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544; 143;	is (s ge 03 ; Gal ry pa		QTSLHF	ISIEGV : :	-WNLNKFTGVIGAFNCQGGGW- :: : PTDIRVFHRVLKELDEMNETWV	VLPDGS	CTDPSGDPNGTEWLQGCHMVHCANDSL 	-KHFKGNGV GSHEVMNRV	-LHAHLEKVGIDGVKIDVIHLLE 	EDLAVI	.GQKGMK	PGLVLID-DGWQSI :: : : -GMMLQRFEYWDKV	KIVRTI
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e :	492	661	442	610	389	570	331	513	287	471	227	444	175	387
Search completed: April 4, 2003, 11:13:33 Job time : 57 secs	DEFQELVFYINWSQKLIDNNLN 513	LILSKPSQDLDIALDPFEFELITVSPVTKLIQTSLH 696	DQIDQENSVLSWYKKVIDLRNNPKIRSTIIQGDFELIADEDPNIFAYKRK- 491	1 1 1 1 1 1	QKIMTHNDFMKLSSIFSRDNARTPIP-WNSKGGENDSGKSWLPYNKSFKTINVE 441	TRDCLFEDPL	DFLDQKAKAFALTLHGLKGTPFIYQGEEIGMDNSDHTNDISKINDVNDLRTYEYHVLK 388	DMFQSTHPCAAFHAASRAISGGP-IYVSDSVGKHNFDLLKKL-VLPDGSILRS-EYYALP 569	GFDFIKFKKIIAQWQKDVSNGWNSLYFNNHDQPRAISRFLHDQV 330	GDDEWCTDPSGDPNGTFWLQGCHMVHCANDSLWMGNFIHPDW 512	LROKTWKDDNEIMSVSESWAMNSKDVNENTNLENKAYSLTFNFDHMISEFEYVDGKKTWK 286	GNGVIASMEHCNDEMELGTEAISL	DEFVEIINFWLDK-GVDGFRFDAFDEIGKPTDLFTRENFYEHDKKFVIEKFKE 226	EEMYEGLHAHLEKVGIDGVKIDVIHLLEMLCEDYGGRVDLAKAYYKAMTKSINKHFK- 443

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Pred. No. is the number of results predicted by score greater than or equal to the score of the and is derived by analysis of the total score di / chance to have a being printed,

SUMMARIES

10	9	8	7	6	ហ	4	ω	N	1	Result No.
2834	2852	2854.5	2854.5	2854.5	2860.5	2945	2996.5	4225	4225	Score
67.1	67.5	67.6	67.6	67.6	67.7	69.7	70.9	100.0	100.0	Query Match Length DB
780	758	781	781	781	783	783	777	784	784	ength
22	21	22	20	19	20	23	20	20	19	DB
AAB98659	AAY70978	AAB49400	AAY30143	AAW57887	AAY32073	ABB93664	AAY32074	AAY17417	AAW53570	ID
Soybean protein: S	Soybean raffinose	Soybean raffinose	Amino acid sequenc	Soybean raffinose	Sugarbeet raffinos	Herbicidally activ	Mustard raffinose	Cucumber raffinose	Cucumber raffinose	Description

Claim 3; Pages 17-20; 26pp; Japanese

Raffinose synthase gene - useful for preparation of raffinose in transformed plant

WPI; 1998-264858/24. N-PSDB; AAV22250.

		•		•	1	ESULT 1 AW53570
	ALIGNMENTS					
human	ABG14554	22	1372		106	45
Ø	AAM00803	22	1080	•	106	44
Rat CARD-6 protein	AAB20088	22	905		106.5	43
lus	AAW09043	18	1174		107	42
B.t. toxin 81A2.	AAR89494	17	1174		107	41
B.thuringlensis to	AAR08257	11	1174		107	
Lettuce pest resis	AAU95482	23	æ	٠	107	39
resis	AAW64169	19	488	2.5	107	38
	AAU95497	23	487	2	107	37
	AAW64182	19	487	2	107	36
Photorhabdus lumin	AAY33727	20	1584	2	107.5	35
<	AAW21636	18	1390	ν.	109	34
Novel toxin expres	AAR25825	13	1174	2.	111	33
4	ABP35067	23	63	ω	153	32
Arabidopsis thalia	AAG28630	21	120	4.	177.5	31
	AAY17422	20	30		181	30
+	AAW53567	19	30	<u>.</u>	181	29
Arabidopsis thalia	AAG28629	21	193	6.	263.5	28
dopsis	AAG28628	21	229	9.	389.5	27
Amino acid sequenc	AAY30145	20	271	18.	788	26
ш,	AAW57889	19	271	18.	788	25
ean raffin	AAY32072	20	265	20.	873	24
raffinose s	AAY70974	21	508	22.	940	23
_	AAY70976	21	770	32.	1384	22
an raffinose	AAY17418	20	750	3 3	1394	21
t raffinose	AAY70981	21	841	<u>ဒ</u> မ	1398.5	20
	AAY70975	21	756	33	1432.5	19
sy	AAY70977	21	763	34.	1470	18
)Se	AAY70980	21	751	35.	1490	17
Herbicidally activ	ABB92806	23	807	43.	1853.5	16
Rapeseed raffinose	AAY32075	20	572	56.	2364	15
₩.	AAY30144	20	587	59.	2529	14
ese ar	5788	19	587	59.	2529	13
Amino acid sequenc	AAY30142	20	799	65.	2767	12
Broad bean raffino	AAW57886	19	799	65.	2767	11

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26-APR-1996;
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                                                                                                   661
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EYLF
                                               GGRVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLGTEAISLGRVGDDFWCTDPS
                                                                                                             LILSKPSQDLDIALDPFEFELITVSPVTKLIQTSLHFAPIGLVNMLNTSGAIQSVDYDDD
                                                                                                                                                                FNCQGGGWCRETRRNQCFSQYSKRVTSKTNPKDIEWHSGENPISIEGVKTFALYLYQAKK
                                                                                                                                                                                                                SVGKHNFDLLKKLVLPDGSSILRSEYYALPTRDCLFEDPLHNGETMLKIWNLNKFTGVIGA
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                                                                                                                                                   FNCQGGGWCRETRRNQCFSQYSKRVTSKTNPKDIEWHSGENPISIEGVKTFALYLYQAKK
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RESULT 2 AAY17417 ID AAY1

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Matches 784
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30-APR-1998;
04-DEC-1998;
10-DEC-1998;
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                 This sequence represents mustard raffinose synthase, a protein that can bind a D-galactosyl group through an alpha(1-6) bond thydroxy group attached to the carbon atom at the 6-position of D-glucose residue in a sucrose molecule to form raffinose. CDN (see AAZ20209) encoding the enzyme was isolated from mustard
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                                                                                                                                               NKETGVIGAFNCQGGGWCRETRRNQCFSQYSKRVTSKTNPKDIEWHSGENPISIEGVKTF
                                                                                                                                                                                                                           DDFWCTDPSGDINGTYWLQGCHMVHCAYNSLWMGNFIQPDWDMFQSTHPCAEFHAASRAI
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SAPEGLSSIKYEF
                     SSSGGISVIEYLF
                                                        IQSVDYDDDLSSVEIGVKGCGEMRVFASKKPRACRIDGEDVGFKYDQDQMVVVQVPWPID
                                                                                                                                  NKYTGIIGAFNCQGGGWCRETRRNQCFSQCVNTLTATTNPKDVEWNSGNNPISVENVEEF
                                                                                                                                                                                                                                                                                                                   IVRPELSPGLKLTMQDLAVDKIVDTGIGFVSPDMANEFYEGLHSHLQNVGIDGVKVDVIH
                                            IRSLVYHEE --
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Pred. No. 2.5e-274;
9; Mismatches 114;
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                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant
                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                               greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequence from plant with nucleic acid or amino acid sequences from non-plant
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K - - - :
                                               SFDGLN--DMSSPFAIDGSDFTVNGHSFLSDVPENIVASPSPYTSIDKS----PVSVGCF
                                                                                                                                                                                                           VGFDA-SEPDSRHVVSIGKLKDIRFMSIFRFKVWWTTHWVGRNGGDLESETQIVILEK-- 124
                      KATGPRAGQKGMKAFIDELKGEFKTVEHVYVWHALCGYWGGLRPQVPGLPEARVIQPVLS
                                                                                                                                              SDSGPGSGSGRPYVLLLPLLEGSFRSSFQSGEDDDVAVCVESGSTEVTGSEFRQIVYVHA
                                                                                                                                                           -----SDSGRPYVFLLPIVEGPFRTSIQPGDDDFVDVCVESGSSKVVDASFRSMLYLHA 178
                                                                                                                                                                                                                                             SDSGINGVDFTEKFRLEDSTLLANGQVVLTDVPVNVTLTSSPYL-VDKDGVPLDVSAGSF
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                                                                                                                                                                                              IGFNLDGEPKSHHVASIGKLKNIRFMSIFRFKVWWTTHWVGSNGRDIENETQIIILDQSG
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                                                                                                                                                                                                                                                                                                         Similarity
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DQNDVGMKAFVRDLKDEFSTVDYIYVWHALCGYWGGLRPEAPALPPSTIIRPELS
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                                                                                                                                                                                                                                                                                                                                               783 AA;
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Pred. No. 1.9e-269;
9; Mismatches 117;
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30-APR-1998;
04-DEC-1998;
10-DEC-1998;
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                    N-PSDB; AAZ20208
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                                                                                                                                                                                                          Misc-difference
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348
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LNKFTGVIGAFNCQGGGWCRETRRNQCFSQYSKRVTSKTNPKDIEWHSGENPISIEGVKT
                                                                                                                                                                                                                                                                               QVVTPKLSPGLEMTMEDLAVDKIVNNGIGLVQPDKAQELYEGLHSHLENCGIDGVKVDVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIDKSPVSVGCFVGFDASEPDSRHVVSIGKLKDIRFMSIFRFKVWWTTHWVGRNGGDLES 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAPSFSKENSKTCDEVANHDDCN--TCPIISLEESNFMVNGHVILSQVPSNI----T
                                                       LNKYNGVLGVFNCQGGGWSRESRKNLCFSEYSKPISCKTSPKDVEWENGHKPFPIKGVEC
                                                                                                             ISGGPIYVSDVVGKHNIPLLKRLVLADGSILRCEYHALPTKDCLFVDPLHDGKTMLKIWN
                                                                                                                                         ISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALPTRDCLFEDPLHNGETMLKIWN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 31-34; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid molecule encoding plant raffinose synthetase capable of producing raffinose, used as food additives with beneficial effects on gastrointestinal flora
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                                                                                                                                                                                                                             MAPSI----SKTVELNSFGLVNGNLPLSITLEGSNFLANGHPFLTEVPENIIVTPSP---
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          WPI; 1999-511112/43
N-PSDB; AAZ10002.
                                                                                                             JP11215984-A
                                                                                                                                                                                                               AAY30143 standard;
                                                  28-NOV-1997;
18-DEC-1996;
                                                                                                                                              Raffinose
                                                                                                                                                              Amino acid sequence
                                                                                                                                                                               26-OCT-1999
                                                                            12-DEC-1997;
                                  (SUMO ) SUMITOMO CHEM
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WP---SASKLSMVEFLF 781
                                                                                                                                                                                                                                                                                                                         TGGAIQSMEFDNHIDVVKIGVRGCGEMKVFASEKPVSCKLDGVVVKFDY-EDKMLRVQVP
                                                                                                                                                                                                                                                                                                 TSGAIQSVDYDDDLSSVEIGVKGCGEMRVFASKKPRACRIDGEDVGFKYDQDQMVVVQVP
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                                                  97JP-0329006.
96JP-0338673.
                                                                            97JP-0342899
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                                                                                                                                                             of a raffinose synthase protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New raffinose synthase gene -
768
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                        WPIDSSSGGISVIEYLF
                                                                  TSGAIQSVDYDDDLSSVEIGVKGCGEMRVFASKKPRACRIDGEDVGFKYDQDQMVVVQVP
                                                                                                                        VKTFALYLYQAKKLILSKPSQDLDIALDPFEFELITVSPVTKLIQTSLHFAPIGLVNMLN : ||:||:| | : : : |||||||||||
                                                                                                                                                                                                                                SRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALPTRDCLFEDPLHNGETMLK
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                                                                                                        MNVFAVYLFKDHKLKLMKASEKLEVSLEPFTFELLTVSPVIVLSKKLIQFAPIGLVNMLN
                                                                                                                                                                                       IWNLNKFTGVIGAENCQGGGWCRETRRNQCFSQYSKRVTSKTNPKDIEWHSGENPISIEG
                                                                                                                                                                                                                     SRAISGGPVYVSDCVGKHNFKLLKSLALPDGTILRCQHYALPTRDCLFEDPLHDGKTMLK
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                                                     TGGAIQSMEFDNHIDVVKIGVRGCGEMKVFASEKPVSCKLDGVVVKFDY-EDKMLRVQVP
                                                                                                                                                               IWNLNKYTGVLGLFNCQGGGWCPVTRRNKSASEFSQTVTCLASPQDIEWSNGKSPICIKG
                                                                                                                                                                                                                                                                                                                                                                                                                                       ENYKFRQYCSGKDS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENYKFRDYVNPKATGPRAGQKGMKAFIDELKGEFKTVEHVYVWHALCGYWGGLRPQVPGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ID-KSPVS-----VGCFVGFDASEPDSRHVVSIGKLKDIRFMSIFRFKVWWTTHWVGRN 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  al Similarity
525; Conserv
SASKLSMVEFLF
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                                                                                                                                                                                                                                                                                                                                                                                                                 New soybean plant promoters useful for generating with desired properties -
                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
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01-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                   present invention provides novel plant promoters which can be used production of transgenic plants which express genes with desired
                                                                                                                                                                                                                                                                      MAPSFKNGGSNVVSFD--GLNDMSSPFAI--DGSDFTVNGHSFLSDVPENIVASPSPYTS 56
                                                       MAPSI----SKTVELNSFGLVNGNLPLSITLEGSNFLANGHPFLTEVPENIIVTPSP--- 53
                  PQGVIEGVRHLVDGGCPPGLVLIDDGWQSIGHDSDPIT-KEGMNQTVAGEQMPCRLLKFQ
                                                                                                                                                 SFRSMLYLHAGDDPFALVKEAMKIVRTHLGTFRLLEEKTPPGIVDKFGWCTWDAFYLTVH 228
                                                                                                                                                                             GHELEHETQMMLLDKNDQLGRPFVLTLPTLQASFRASLQPGLDDYVDVCMESGSTRVCGS
                                                                                                                                                                                                GGDLESETQIVILEKSDS-GRPYVFLLPIVEGPFRTSIQPGDDDFVDVCVESGSSKVVDA 168
                                                                                                                                                                                                                              ID-KSPVS-----VGCFVGFDASEPDSRHVVSIGKLKDIRFMSIFRFKVWWTTHWVGRN 109
DVIHLLEMICEDYGGRVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLGTEAISL
                                                                                                                                       SFGSCLYVHVGHDPYQLLREATKVVRMHLGTFKLLEEKTAPVIIDKFGWCTWDAFYLKVH
                                                                                                                                                                                                                    IDAKSSKNNEDDDVVGCFVGFHADEPRSRHVASLGKLRGIKFMSIFRFKVWWTTHWVGSN 113
                                                                                                 PSGVWEGVKGLVEGGCPPGMVLIDDGWQAICHDEDPITDQEGMKRTSAGEQMPCRLVKLE
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Pred. No. 7.2e-261;
3; Mismatches 120;
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                 The present sequence is a raffinose synthase from clone sfl1.pk125.d4 isolated from a soybean immature flower cDNA library sfl1. Raffinose synthase is involved in the biosynthesis of raffinose and higher homologues in the raffinose saccharide family from sucrose. The present sequence is useful for reducing the raffinose saccharide content of soybean seeds which improves the nutritional quality of the soy protein products derived from them.
                                                                                                                 Nucleic acids and encoded proteins involved in the biosynthesis raffinose, useful for producing soybean seeds with a reduced raccontent and therefore improved nutritional quality - \frac{1}{2}
                                                                                                Claim 2;
                                                                                                                                                           N-PSDB;
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The present invention relates to a mutant protein of raffinose synthase in which at least one aromatic amino acid present at the position of about 1-7 amino acids from the N-terminus is deleted or replaced. The mutant protein can be used for reducing the raffinose oligosaccharide content in a plant body. The present protein from soybean, was used in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 18-20; 30pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel mutant protein of raffinose synthase is useful for reducing raffinose oligosaccharide content in a plant body \boldsymbol{\cdot}
SRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALPTRDCLFEDPLHNGETMLK
                                                                                                                                                                                                                                                                                                                                GHELEHETQMMLLDKNDQLGRPFVLILPILQASFRASLQPGLDDYVDVCMESGSTRVSGS
                                                                 GRVGDDFWCTDPSGDPNGTFWLQGCHMVHCANDSLWMGNFIHPDWDMFQSTHPCAAFHAA
                                                                                                                                                        DVIHLLEMLSEEYGGRVELAKAYYKALTASVKKHFKGNGVIASMEHCNDFFLLGTEAIAL
                                                                                                                                                                                                                                            PEARVIQPVLSPGLQMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGIDGVKI
                                                                                                                                                                                                                                                                                                                                                                                                                                             PQGVIEGVRHLVDGGCPPGLVLIDDGWQSIGHDSDPIT-KEGMNQTVAGEQMPCRLLKFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SFRSMLYLHAGDDPFALVKEAMKIVRTHLGTFRLLEEKTPPGIVDKFGWCTWDAFYLTVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGDLESETQIVILEKSDS-GRPYVFLLPIVEGPFRTSIQPGDDDFVDVCVESGSSKVVDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAPSI----SKTVELNSFGLVNGNLPLSITLEGSNFLANGHPFLTEVPENIIVTPSP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAPSFKNGGSNVVSFD--GLNDMSSPFAI--DGSDFTVNGHSFLSDVPENIVASPSPYTS
                                                                                                                                                                                                 DVIHLLEMLCEDYGGRVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLGTEAISL
                                                                                                                                                                                                                                                                                                                                                                                                                       PSGVWEGVKGLVEGGCPPGMVLIDDGWQAICHDEDPITDQEGMKRTSAGEQMPCRLVKLE
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Pred. No. 6.3e-259;
21; Mismatches 120;
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                                 Query Match
Best Local S
Matches 508
                                                                                                  This sequence represents the broad bean raffinose synthetase of the invention. The raffinose synthetase is capable of producing raffinose by combining a D-galactosyl group through an alpha (1-6) bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule. The DNA can be used to modify metabolism of a host organism by introducing into the host organism or its cell so that the content of the raffinose family oligosaccharides in the host organism or cell is changed. Raffinose oligosaccharides are useful as food additives with beneficial effects on the gastrointestinal flora.
                                                                               Sequence
                                                                                                                                                                                                                    Claim 1; Page
                                                                                                                                                                                                                                          New nucleic acid molecule encoding plant raffinose synthetase capable of producing raffinose, used as food additives with beneficial effects on gastrointestinal flora
                                                                                                                                                                                                                                                                                         N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Raffinose synthetase; metabolism modification; gastrointestinal flora; broad bean.
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1998-324670/29.
DB; AAV40800.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WP---SASKLSMVEFLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SRAISGGPIYVSDCVGKHNFKLLKSLALPDGTILRCQHYALPTRDCLFEDPLHDGKTMLK
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                                             Similarity
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                                  Conservative
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                                Score 2767; DB 19;
Pred. No. 1.5e-252;
8; Mismatches 140;
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                                  JP11215984-A
                                                                            Raffinose synthase;
                                                                                                    Amino acid
                                                                                                                           26-OCT-1999
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            10-AUG-1999
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                                                                                                                                                                                                                                                                                         AIQSVDYDDDLSSVEIGVKGCGEMRVFASKKPRACRIDGEDVGFKYDQDQMVVVQVPWPI 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVIEGVRHLVDGGCPPGLVLIDDGWQSIGHDSDPITKEGMNQTVAGEQMPCRLLKFQENY 290
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                                                                                                                                                                                                                               --SSSTLSLVQFLF
                                                                                                                                                                                                                                                      DSSSGGISVIEYLF 784
                                                                                                                                                                                                                                                                                                                                                                                             LNKFTGVIGAFNCQGGGWCRETRRNQCFSQYSKRVTSKTNPKDIEWHSGENPISIEGVKT
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                                                                                                                                                                                                                                                                                                                          FAVYFFKEKKLRLMKCSDRLKVSLEPFSFELMTVSPVKVFSKRFIQFAPIGLVNMLNSGG
                                                                                                                                                                                                                                                                                                                                                                        LNKYTGVLGLFNCQGGGWCPEARRNKSVSEFSRAVTCYASPEDIEWCNGKTPMSTKGVDF
                                                        faba
                                                                                                                                                                        standard;
                                                                                                    sequence of a raffinose synthase
                                                                                                                          (first entry)
                                                                                                                                                                        Protein;
                                                                              plant;
                                                                               broad
                                                                               bean;
                                                                               sucrose; raffinose.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New raffinose synthase gene - is prepared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-NOV-1997;
18-DEC-1996;
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                                                                        LNKFTGVIGAFNCQGGGWCRETRRNQCFSQYSKRVTSKTNPKDIEWHSGENPISIEGVKT
                                                                                                                                                                                           GDDFWCTDPSGDPNGTFWLQGCHMVHCANDSLWMGNFIHPDWDMFQSTHPCAAFHAASRA
                                                                                                                                                                                                                                                     HLLEMLCEDYGGRVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLGTEAISLGRV
                                                                                                                                                                                                                                                                                            RVVVPKVSQGLKMTMEDLAVDKIVENGVGLVPPDFAHEMFDGLHSHLESAGIDGVKVDVI
                                                                                                                                                                                                                                                                                                            RVIQPVLSPGLQMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGIDGVKIDVI 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RSMLYLHAGDDPFALVKBAMKIVRTHLGTFRLLEEKTPPGIVDKFGWCTWDAFYLTVHPQ
                            FALYLYQAKKLILSKPSQDLDIALDPFEFELITVSPVTKLIQTSLHFAPIGLVNMLNTSG
                                                                                                                                              ISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALPTRDCLFEDPLHNGETMLKIWN 590
                                                                                                                                                                           GDDFWCSDPSGDPNGTYWLQGCHMVHCAYNSLWMGNFIQPDWDMFQSTHPCAEFHAASRA
                                                                                                                                                                                                                                    HLLELLSEEYGGRVELARAYYKALTSSVKKHFKGNGVIASMEHCNDFFLLGTEAISLGRV
                                                                                                                                                                                                                                                                                                                                                   KFREYENPE----NGGKKGLGGFVRDLKEEFGSVESVYVWHALCGYWGGVRPGVHGMPKA
                                                                                                                                                                                                                                                                                                                                                                                KERDYVNPKATGPRAGQKGMKAFIDELKGEFKTVEHVYVWHALCGYWGGLRPQVPGLPEA
                                                                                                                                                                                                                                                                                                                                                                                                              GVWEGVKSLTDGGCPPGFVIIDDGWQSICHDDDDEDDSGMNRTSAGEQMPCRLVKYEENS
                                                                                                                                                                                                                                                                                                                                                                                                                                        GVIEGVRHLVDGGCPPGLVLIDDGWQSIGHDSDPITKEGMNQTVAGEQMPCRLLKFQENY 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELQHETQMLILDKNDSLGRPYVLLLPILENTFRTSLQPGLNDHIGMSVESGSTHVTGSSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DLESETQIVILEKSDS-GRPYVFLLPIVEGPFRTSIQPGDDDFVDVCVESGSSKVVDASF 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DVISTIDIGNGNSPLFSITLDQSRDFLANGHPFLTQVPPNITTTTTTTASSFLNLKSNKD
FAVYFFKEKKLRLMKCSDRLKVSLEPFSFELMTVSPVKVFSKRFIQFAPIGLVNMLNSGG
                                                         LNKYTGVLGLFNCQGGGWCPEARRNKSVSEFSRAVTCYASPEDIEWCNGKTPMSTKGVDF
                                                                                                                   1SGGP1YVSDCVGNHNFKLLKSLVLPDGS1LRCQHYALPTRDCLFEDPLHNGKTMLKIWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KACLYIHLSNDPYSILKEAVKVIQTQLGTFKTLEEKTAPSIIDKFGWCTWDAFYLKVHPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 19-21; 40pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97JP-0329006.
96JP-0338673.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 2767; DB 20; Pred. No. 1.5e-252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from a plant material
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     799;
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                                                                                      650
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                                                         669
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RESULT 13
AAW57888
ID AAW57
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                                                                                                              Db
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                                                                                                                                                                    Best Local Similarity
Matches 448; Conserv
                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                  This sequence is the Japanese artichoke raffinose synthetase of the invention. The raffinose synthetase is capable of producing raffinose by combining a D-galactosyl group through an alpha (1-6) bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule. The DNA can be used to modify metabolism of a host organism by introducing into the host organism or its cell so that the content of the raffinose family oligosaccharides in the host organism or cell is changed. Raffinose oligosaccharides are useful as food additives with beneficial effects on the gastrointestinal flora.
                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid molecule encoding plant raffinose synthetase capable of producing raffinose, used as food additives with beneficial effects on gastrointestinal flora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Raffinose synthetase; metabolism modification; gastrointestinal flora; Japanese artichoke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stachys sieboldii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Japanese artichoke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW57888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW57888 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-DEC-1997;
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121
                           229
                                                                                   169
                                                                                                                                           109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SUMO ) SUMITOMO CHEM CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          788
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                                                       61
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              PQGVIEGVRHLVDGGCPPGLVLIDDGWQSIGHDSDPITKEGMNQTVAGEQMPCRLLKFQE
                                                                        SFRSMLYLHAGDDPFALVKEAMKIVRTHLGTERLLEEKTPPGIVDKFGWCTWDAFYLTVH 228
                                                                                                                                          NGGDLESETQIVILEKSDSGRPYVFLLPIVEGPFRTSIQPGDDDFVDVCVESGSSKVVDA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AIQSLEFDDNASLVKIGVRGCGEMSVFASEKPVCCKIDGVKVKFLY-EDKMARVQILWP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AIQSVDYDDDLSSVEIGVKGCGEMRVFASKKPRACRIDGEDVGFKYDQDQMVVVQVPWPI
                                                       SFRASLYMHAGDDPFTLVKDAVKVARHHLGTFRLLEEKTPPGIVDKFGWCTWDAFYLNVQ
                                                                                                               NGSDLERETQIVVLDKSDD-RPYIVLLPLIEGQFRASLQPGVDDFIDICVESGSTKVNES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DSSSGGISVIEYLF
PHGVMEGVQGLVDGGCPPGLVLIDDGWQSICHDNDALTTEGMGRTSAGEQMPCRLIKFEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSSTLSLVQFLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV40802
                                                                                                                                                                                                                                                                                                                                                                                                Page 36-38; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wantanabe
                                                                                                                                                                                                                             587 AA;
                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      raffinose
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                                                                                                                                                                                 59.9%;
                                                                                                                                                                       62;
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                                                                                                                                                                                Score
Pred.
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                                                                                                                                                                       Mismatches
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No. 3.
                                                                                                                                                                                    No.
                                                                                                                                                                      :.2e-230;
ies 70;
                                                                                                                                                                                                 DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           food additive;
                                                                                                                                                                       Indels
                                                                                                                                                                                                 Length
                                                                                                                                                                                                    587;
                                                                                                                                                                                                                                                                                                                                                      e of the raffinose by
                                                                                                                                                                       2;
                                                                                                                                                                      Gaps
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RESULT 14
AAY30144
ID AAY30144
AAY AAY30
AX AAY30
AAY30
AAY30144
A
                                                                               Query Match
Best Local
                                                       Matches
                                                                                                                                                            Sequence
                                                                                                                                                                                                      The present sequence represents a raffinose synthase protein. sequence is isolated from plant material. The protein forms resequence is isolated from blant material hydroxyl group of the complexing alpha(1 to 6). D-galactosyl hydroxyl group of the D-glucose residue in sucrose molecules.
                                                                                                                                                                                                                                                                                                                                        Claim 12;
                                                                                                                                                                                                                                                                                                                                                                                   New raffinose synthase gene - is prepared
                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AA210003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-511112/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-NOV-1997;
18-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Raffinose synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of a raffinose synthase protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY30144;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           289
  109 NGGDLESETQIVILEKSDSGRPYVFLLPIVEGPFRTSIQPGDDDFVDVCVESGSSKVVDA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARVIQPVLSPGLQMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGIDGVKID 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WNLNKFTGVIGAFNCQGGGWCRETRRNQCFSQYSKRVTSKTNPKDIEWHSGENPISIEGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALPTRDCLFEDPLHNGETMLKI 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVGDDFWCTDPSGDPNGTFWLQGCHWVHCANDSLWMGNFIHPDWDMFQSTHPCAAFHAAS 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VIHLLEMICEDYGGRVDLAKAYYKALSSSVNNHFNGNGVIAGLEHCNDFMFLGTEAITLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NYKFRDYVNPKATGPRAGQKGMKAFIDELKGEFKTVEHVYVWHALCGYWGGLRPQVPGLP 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KTFALYLFHEKKLVLSKPSDKIDITLEPFDFELITVSPVKTL 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KTFALYLYQAKKLILSKPSQDLDIALDPFEFELITVSPVTKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WNYNKFTGVVGTFNCQGGGWSREVRRNQCAAEYSHAVSSSAGPSDIEWKQGTSPIDVDGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VIHLLEMLCEDYGGRVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLGTEAISLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NYKFREYESPNKTGP-GPNTGMGAFIRDMKDNFKSVDYVYVWHALCGYWGGLRPNVPGLP
                                                       al Similarity
448; Conserv
                                                                                                                                                                                                                                                                                                                                Page 30-31; 40pp; Japanese.
                                                                                                                                                            587 AA;
                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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96JP-0338673.
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                                                                               59.98;
77.08;
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                                                       62;
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                                                  Score 2529; DB 20;
Pred. No. 3.2e-230;
2; Mismatches 70;
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                                                                                                                                                                                                                                                                                                                                                                                     from a
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                                                       Indels
                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                           material
                                                                                                          587;
                                                                                                                                                                                                                                 raffinose
the 6C
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                                                                                                                                                                                                                                                                                   The
                                                  Gaps
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                                                       2
RESULT 15
AAV32075
ID AAV32
XX
AC AAV32
XX
DT 17-JF
XX
DE Rape:
XX
C Rape:
XX
C Raff
X
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Misc-difference 144
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Misc-difference 132
                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
Misc-difference 129
     30-APR-1998;
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                                                                                                                                                                                                                                 Misc-difference
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Best Local S
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04-DEC-1998;
10-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                 TVSPVTKLIQTSLHFAPIGLVNMLNTSGAIQSVDYDDDLSSVEIGVKGCGEMRVFASKKP 742
                                                                                  KRVTSKTNPKDIEWHSGENPISIEGVKTFALYLYQAKKLILSKPSQDLDIALDPFEFELI 682
TVSPVVTIEGSSVQFAPIGLVNMLNTSGAIRSLVYHEE--SVEIGVRGAGEFRVYASKKP
                                                                                                                                                  SEYYALPTRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCOGGGWCRETRRNQCFSQYS 622
                                                                                                                                                                                                                   WMGNFIHPDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILR 562
                                                                                                                                                                                                                                                                                    KGNGVIASMEHCNDFMFLGTEAISLGRVGDDFWCTDPSGDPNGTFWLQGCHMVHCANDSL 502
                                                                                                                                                                                                                                                                                                                                                    PEKABEMYEGLHAHLEKVGIDGVKIDVIHLLEMLCEDYGGRVDLAKAYYKAMTKSINKHF 442
                                                                                                                                                                                                                                                                                                                                                                                                                     TVEHVYVWHALCGYWGGLRPQVPGLPEARVIQPVLSPGLQMTMEDLAVDKIVLHKVGLVP 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DPITKEGMNQTVAGEQMPCRLLKFQENYKFRDYVNPKATGPRAGQKGMKAFIDELKGEFK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1999-593144/51.
DB; AAZ20210.
                                                                  NTLTATTNPNDVEWNSGNNPISIENVEEFALFLSQSKKLVLSGQNDDLEITLEPFKFELI
                                                                                                                                 CEYYALPTRDRLFEDPLHDGKTMLKIWNLNKYTGIIGAFNCQGGGWCRETRRDQCFSQCV
                                                                                                                                                                                                  WMGNFIQPDWDMFQSTHPCAEFHAASRAISGGPIYISDCVGQHDFDLLRRLVLPDGSILR
                                                                                                                                                                                                                                                                   DGNAVIASMEHCNDFMFLGTEAISLGRVGDDFWCTDPSGDINGTYWLQGCHMVHCAYNSL
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                                                                                                                                                                                                                                                                                                                                                                                                  TVDYIYVWHALCGYWGGLRPGAPTLPPSTIVRPELSPGLKLTMQDLAVDKIIDTGIGFVS
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98JP-0345590.
98JP-0351246.
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73.9%;
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Pred. No. 1.3e-214;
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Search completed: April 4, 2003, 11:11:09
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Title:
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 Score
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 GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
 Length
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NAC1_RAT
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P28371 P22427 P46197 P19711 P19701 Q19508 Q00808 P53355 P53355
synechocyst equine infe bos taurus bovine virs herpetosiph influenza a caenorhabdi podospora a homo sapien homo sapien

RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., RA Holroyd S., Hornsby T., Walsh R., Nibbirt D., Odell C., RA RA Chefford K., Rutter S., Saunders D., Seeger K., Sharp S., RA Ratherford K., Rutter S., Saunders D., Seeger K., Sharp S., RA Ratherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., RA Moodward J., Volckaert G., Aert R., Robben J., Gromonprez B., RA Woodward J., Volckaert G., Aert R., Robben J., Gromonprez B., RA Galler E., Vanstreels E., Rieger N., Schaefer M., Meller Auer S., Gabel C., Fuchs M., Fritze C., Holzer E., Moeset D., Hilbert H., RA Borzym K., Langer I., Beck A., Lchrach H., Reinhardt R., Pohl T.M., Ra Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Wedler H., Wambutt R., Purnelle B., RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., McCombie W.R., Paulsen I., Potashkin J., Forsburg S.L., Kan Lucas M., Rochet M., McCombie W.R., Paulsen I., Potashkin J., Forsburg S.L., Warther M., Walshing C., Hunt C., Moore K., Hurst S.M., Thompson S., Armstrong J., Forsburg S.L., Kan Lucas M., Rochet M., Rochet M., Paulsen I., Potashkin J., Forsburg S.L., Walshing M., Walshing M., Potashkin J., Forsburg S.L., Lower M., McCombie W.R.,

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Best Local S
Matches 139
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REPEAT
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RLDD--
                                                                                           DDFGIRIVDVQTRKIVRELWGHSNRLTSFDFSDTGRWLVTASLDGTIRTWDLPTGHLIDS
                                                                                                                                          KPVTAVMLDNVNRILVTASLDGILKFWDFNKGNLIDSLDVGSSITHAIYQHSSDLVAVAC
                                                                                                                                                                                         QHVLPTSDGTSVRSVCVSCCGNFGLIGSSKGVVDVYNMQSG-----IKRKSFGQSSLSG
                                                                                                                                                                                                                                                            DGSIL----RSEYYALP-----TRDCLFEDPL--HNGETMLKIWNLNKFT--
                                                                                                                                                                                                                                                                                                                                                          D-DFWCTDPSGDPNGTF------WLQGCHMVHCA--NDSL--WM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                 NTNADITSLLHPSTYLNKILLGFSDGALQIWNLRVSKRVHEFQEFFG-DGITSLTQAPVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVEQEHGTVTHLDAFGEWIIACTSSRHVYVWKHASKY-----SVPE---LHTTFLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELKGEFKTV-----EHVYVWHALCGYWGGLRPQVPGLPEARVIQPVLSP 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVGNTFQTYDCEKLNLLFVGKQLDKEITCLK---SFKDFMLVAAGSKIFAYKRGKIIWDI 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGHDSDPITKEGMNQTVAGEQMPCRLLKFQENYKFRDYVNPKATGPRAGQKGMKAFID- 315
                      RIDGEDVGFKYDQDQMVVVQVPWPIDSSSGGISVIE
                                               ISTPSVCTSLTFAPTG.
                                                                    -----TSLHFAPIGLVNMLNTSGAIQSVDYDDDLSSVEIGVKGCGEMRVFASKKPRAC
                                                                                                                                                                   KRVTS----KTNP-----
                                                                                                                                                                                                                                       QGSVISKAKKLNVRPEELKLPEITALSSSNTREKYWDNVLTAHKNDSSARTWNWKSKTLG
                                                                                                                                                                                                                                                                                      RSRNGHYEPPSFVKFYGKSVHFLISAATDRSLRAVS---LY-QDS
                                                                                                                                                                                                                                                                                                             ----GNFIHPDWDMF--QSTH--PCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLP
                                                                                                                                                                                                                                                                                                                                   DLSFWDLSKRRIQNVTYNAHFGSLPKIQFLNGQPILVTAGPDNSLKEWIFDSMDGAPRIL
                                                                                                                                                                                                                                                                                                                                                                                  DVLAVGTISGRI ----VIFNLKNGSILMEFKQDGQVLSCSFRTD----GTPILASSNPIG
                                                                                                                                                                                                                                                                                                                                                                                                         EMLC-EDYGGRVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLGTEAI-SLGRVG 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLQMTMEDLAVDKIVLHKVGLVPPEKAEEMY - - - - EGLHAHLEKVGIDGV - KIDVIHLL 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00400;
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100569 MW;
---VVEVSAPSVSGEKGISVVE 678
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Pred. No. 0.35;
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                                                                                                                                                                 KDIEWHSGENPISIEGVKTFALYLYQAKKLILSKPS
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SEEFFC6034BDC047 C
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                                                                                                                                                                                                                -GVIGAFNCQGGGWCRETRRNQCFSQYS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRC64;
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Best Local !
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Q03745;
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pesticidial crystal protein crylEb (Insecticidal CryIE(b)) (Crystaline entomocidal protoxin) (134 CRYIEB OR CRYIE(B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001178; Endotoxin.
Pfam; PF00555; endotoxin; 1.
Toxin; Sporulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. The further content is in no way use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genes encoding lepidopteran-active toxins and transformed hosts.", Patent number US5206166, 27-APR-1993.

-i- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Toxin; Sporulation. SEQUENCE 1174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M73253; AAA22346.1; HSSP; P02965; 1CIY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPITHELIAL CELLS OF MANY LEPIDOPTERAN LARVAE.

-!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-NRRL B-18457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus thuringiensis (subsp. aizawai) Bacteria; Firmicutes; Bacillales; Bacil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OF THE SPORE COAT.
-!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Payne J.M., Sick A.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1433;
                 809
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                                                                                                                   546
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                                                                                                                                                                                                                                                                                                                                                         373
                                                                                                                                                                                                                                                                                                                                                                                                                        336 YWGGLR------PQVPGLPE-----ARVIQPVLSPGLQMTMEDLA-----VDK 372
                                                                                                                                                                                                                                                                                                                                                                                       314 YWAGHRVTSHFTGSSQVISSPQYGITANAEPSRTIAPSTFPGLNLFYRTLSDPFFRRSDN 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-TERMINUS.
WCRETRRNQCFS-QYSKRVTSKTN-:|::|
                                                                                                                                                                                                                                                                                     GRVDLAKAYYKAMTKSI ---
                                                                                                                                                                                                                                                                                                                                                      I------VLHKVGLVPPEKAEEMY--EGLHAHLEKVGIDGVK--IDVIHLLEMLCEDYG
                                                                                                                   TMSANGSLTSQSFRFAEFPVGIST - - -
                                                                                                                                                  VHCANDSLWMGNFIHPDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLV
                                                                                                                                                                                     FTGGDIIRTNVNGNVLSMSLNFSNTSLQRYRVRVRYAASQTMVMRVNVGGSTTFDQGFPS
                                                                                                                                                                                                                                                    SHYTLTRSLYNTNITSLPTFVWTHHSATDRNITYPDVITQIPLVKSFSLTSGTSVVRGPG
                                                                                                                                                                                                                                                                                                                      IMPTLGINVVQGVGFIQPNNGEVLYRRRGTVDSLDELPIDGENSLVGYSHRL------
                                                IPVDATFEAEYDLERAQKAVNSLFTS---SNQIELKTDVTDYHIDQVSNLV---DCLSDE
                                                                                  LPDGSILRSEY - - - YALPTRDCLFEDPLHNGETMLKI - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.5%;
19.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                     -NKHFKGNGVIASMEHCNDF-MFLGTEAI-SLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5EEA0BA7FD63480F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1174
                                                                                                                   -SGSQTAG-ISISNNPGRQTFHLDRIEF
                                                                                                                                                                                                                      ----PNGTFWLQGCHM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           181;
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AND AS I
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                 641
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RESULT 3
AIM1_HUMAN
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                                                                                                                                                                                                                                                                        EMBL; U83116;
EMBL; U83115;
HSSP; P02526;
            DOMAIN
DOMAIN
DOMAIN
                                                                                                                            SMART; SM00458; RICIN; 1.
SMART; SM00247; XTALbg; 6.
PROSITE; PS00225; CRYSTALLIN_BETAGAMMA;
                                                                                                                                                                     InterPro; IPR001064; Crystallin.
InterPro; IPR000772; Ricin_B_lectin.
Pfam; PF00030; crystall; 6.
Pfam; PF00052; Ricin_B_lectin; 3.
PRINTS; PR01367; BGCRYSTALLIN.
                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 94:3229-3234(1997).
-I- FUNCTION: MAY FUNCTION AS SUPPRESSOR OF MALIGNANT MELANOMA. I EXERT ITS EFFECTS THROUGH INTERACTIONS WITH THE CYTOSKELETON.
-I- SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY. CONT 6 TANDEM REPEATS OF A BETA/GAMMA-TYPE CRYSTALLIN DOMAIN.
-I- SIMILARITY: CONTAINS 1 RICIN B-TYPE LECTIN DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    superfamily, is associated with the control of tumorigenicity malignant melanoma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AIM1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Absent in melanoma 1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AIM1_HUMAN
                                                                                                                                                                                                                                                MIM; 601797; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97250519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RAY M.E., Wistow G., Su Y.A., Meltzer P.S., Trent J.M.;
"AIM1, a novel non-lens member of the betagamma-crystallin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSPVTKLIQTSLHFAPIGLVNMLNTSGAIQSVDYDDDLS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YVTLPGTFDECYPTYLYQ--KIDESKLKAYNRYQLRGYIEDSQDLEIYLIRYNAKHETVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDRGWRGSTDITIQGGDDVFKEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VPGTGSLWPLSVE-SPIGRCGEPNR--CVPHLEWNPDLDCSCRDGEKCAHHSHHFSLDID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PISIEGV--KTFALYLYQAKKLILSK-------PSQDLDIALDPF--EFELIT
                                                                                                                                                                                                                                                            HGNC:356; AIM1.
               Lectin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=9096375;
1119
1206
1318
1404
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1584
1719
                                                                                                               RICIN_B_LECTIN;
            CRYSTALLIN BETA/GAMMA-LIKE 1
CRYSTALLIN BETA/GAMMA-LIKE 2
CRYSTALLIN BETA/GAMMA-LIKE 3
CRYSTALLIN BETA/GAMMA-LIKE 4
CRYSTALLIN BETA/GAMMA-LIKE 5
CRYSTALLIN BETA/GAMMA-LIKE 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    753
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RESULT 4
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PARE

GLGB_HAEIN P45177; 01-NOV-1995 01-NOV-1995

STANDARD;

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSEDGLNDMSSPFAIDGSDFTVNGHSFLSDVPENIVASPSPYTSIDKSPVSVGCFVGF-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IQDCSSWSLSPVILIKVVRGCWILYEQPNFEGHSIPLEEGELELSGLWGIEDILERHEEA 1102
KSDG--RIYSKLKPNLVLDIKG---GTQYDQNHIIL 1704
                                                                                                                                                                                                                            GVIGAFNCQ------GGGW------
                                                                                                                                                                                                                                                            SAMGCPPGATFKS----LRFIDVEFSEPTIILFEREDFKGKKIELNAETV----NLRSL-
                                                                                                                                                                                                                                                                                                                          QFQGHS-----QSFEETTSQIDDSFSTKSCRVSGGSWVVYDGENFTGNQYVLEEGHYPCL
                                                                                                                                                                                                                                                                                                                                                                                            YK----ISSVQPI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QGFGVMQKTCS-MKVHWGTWLIYEEPGFQGVPFILEPGEYPDLSFWDTEAAYIGSMRPLK 1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --FALVKEAMKIVRTHLGTFRLLEEKTPPGI-----VDKFGWCTWDAFYLTVHP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSGRPYVFLLPIVEGPFRTSIQPGDDDFVDVCVESGSSKVVDASFRSMLYLHAGDDP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISFSGMS-LSDTMTLRGS------VQNKLNPRPGKVVIYSEPDVSEKCIEVFSD 1042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156;
                                KGCGEMRVFASKKPR-ACRIDGEDVGFKYDQDQMVV 763
                                                                                             DLDIALDPFEFELITVSPVTKLIQTSLHFAPIGLVNMLNTSGAIQSVDYDDDLSSVEIGV
                                                                                                                             -- KRIYFRLRNKATGLFMSTNG-NLEDLKLLRIQVMEDVGADDQIWIYQ-EGCIKCRIAE
                                                                                                                                                             YSKRVTSKTNPKDIEWHSGENPISIEGVKTF --
                                                                                                                                                                                                                                                                                           KKLVLPDGSILRSEYYALPTRDCLFEDPL------HNGETMLKIWNLNKFT
                                                                                                                                                                                                                                                                                                                                                          LWMGNFIHPDWDMFQSTHPCA--AFHAASRAISGGPIYVSDS-----VGKHNFDLL
                                                                                                                                                                                                                                                                                                                                                                                                                          FKGNGVIASMEHCNDFMFLGTEAISLGRVGDDFWCTDPSGDPNGTFWLQGCHMVHCANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDVLGIVANLKETGY-GVKTQSINVLSGVWVAYENPDFTGEQYILDKGFYTSFEDWGGKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMYEGLHAHLEKVGIDGVKIDVIHLLEMLCEDY-----GGRVDLAKAYYKAMTKSINKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YVWHALCGYWGGLRPQVPGLPEARVIQPVLSPGLQMTMEDLAVDKIVLHKVGLVPPEKAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VGSMKVLRGIWVA------YEKP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGMNQTVAGEQMPCRLLKFQENYKFRDYVNPKATGPRAGQKGMKAFIDELKGEFKTVEHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASEPDSRHVVSIGKLKDIRFMSIFRFKVWWTTHWVGRNGGDLE-----SETQIVILEKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGGRKVEFPTDPKVVVYEKPFFEGKC----VELETGMCSFVMEGGETEEATGDDHLPFTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                              -GFNTQIRSVQVIGGIWVTYEYGSYRGRQFLLSPAEVPNWYEFSGCRQIGSLRPFVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVVIGSIRHVVQDYRVSHIDLFTEPEGLGILSSYF-----
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7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 106;
Pred. No. 5
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                                                                                                                                                                                                                                                                                                                                                                                          --CLDSFTGPRRR-----NQIHLFSEP
                                                                IVGSLVTSGSKLGLALDQNADSQFWSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -GETGHQYLLEE--GEYRD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -DFSNAHMIMYSEKNFGSKGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ۳
                                                                                                                                                             --- ALYLYQAKKLILSKPSQ
                                                                                                                                                                                                                            -----CRETRRNQCFSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
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Matches
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ACT_SITE
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Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95350630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                     GLycogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rd.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U32815; TIGR; HI1357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 269:496-512(1995).
-!- CATALYTIC ACTIVITY: Formation
                                                             238
                                                                                                                     178
                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000461; Alpha_amylase.
InterPro; IPR004193; Isoamylase_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Whole-genome random sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemophilus influenzae.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2002 (Rel
1,4-alpha-glucan
    289
                                 283
                                                                                          238
                                                                                                                                                  182
                                                                                                                                                                               125
                                                                                                                                                                                                            138
                                                                                                                                                                                                                                         89
                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glycogen.
PATHWAY: Glycogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KNOWN AS THE ALPHA-AMYLASE FAMILY.
NYKFRDYVNPKATGPRAGQKGMKAFIDELKGEFKTVEHVYVWHALCGYWGGLRPQVPGLP
                                                                                                                  AGDDPFALVKEAMKIVRTHLGTFRLLEEKTPPGIVDKFGWCTWDAFYLTVHPQGVIEGVR
                                                                                                                                               ASLGQLYKFELIDCHGNLRLKADPFAFSSQLRPDTASQVSALPNVVEMTEARKKA---
                                                                                                                                                                         SDSGRPYVFLLPIVEG------PFRTSIQPGDDDFVDVCVESGSSKVVDASFRSMLYLH
                                                                                      QGNQP-----ISIYEVHLGSWR-----RNLENNF-WLDYDQIADELIPYVKEMGFT
                                                                                                                                                                                                            VNFRLWAPNARRVSIVGDF-----
                                                                                                                                                                                                                                    VGFDASEPDSRHVVSIGKLKDIRFMSIFRFKVWWTTHWVGRNGG----DLESETQIVILEK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OR HI1357
                                                                                                                                                                                                                                                                    al Similarity
117; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                 PF00128; alpha-amylase; PF02922; isoamylase_N;
                                                                                                                                                                                                                                                                                                                                                                                     proteome.
                                                                                                                                                                                                                                                                                                                                                                                                     biosynthesis;
                                                                                                                                                                                                                                                                                                                           405
458
526
730 AA;
                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC23004.1;
                                                        -VDGGCPPGLVLIDDGWQSIGHDSDPITKEGMNQTVAGEQMPCRLLKFQE
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n branching
                                                                                                                                                                                                                                                                                                                                           405
458
526
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17
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                                                                                                                                                                                                                                                                                                                                                                                                Transferase; Glycosyltransferase;
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                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                           Pred. No. 1.0,
5; Mismatches
                                                                                                                                                                                                                                                                                 Score 105;
Pred. No. 1
                              GYOPLGLYS
                                                                                                                                                                                                                                                                                                                             5B9575317F53769A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and assembly of Haemophilus influenzae
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2.4.1.18) (Glycogen branching
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                                                                                                                                                                                                                                                                                                                             CRC64;
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P19700;
O1-FEB-1991 (Rel. 17, Createu,
O1-FEB-1991 (Rel. 17, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Hemagglutinin precursor [Contains: Hem
"~manalutinin HA2 chain].
                                                 CARBOHYD
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                                                                                                                                                                      Envelope
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-89204912; PubMed=2705304;
Donis R.O., Bean W.J., Kawaoka Y., Webster R.G.;
"Distinct lineages of influenza virus H4 hemagglutinin genes in different regions of the world.";
Virology 169:408-417(1989).
-I- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS CELL RECEPTORS AND FOR INITIATING INFECTION.
                                                                                                                                                                                                                                       InterPro; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutinin; 1.
PRINTS; PR00329; HEMAGGLUTN12.
                           CARBOHYD
                                                                                                                          CHAIN
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HEMA_IARUD
                                                                                                                                                                                                                        ProDom;
                                                                                                                                                                                                                                                                                                                       HSSP;
                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS
(HA1 AND HA2) LINKED BY A DISULFIDE BOND.
-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Influenza A virus (strain A/Ruddy Turnstone/New Jersey/47/85). Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza A viruses; Influenzavirus A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Influenza
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                                                                                                                                                                                                                                                                                                                    G34214; HMIVF7.
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  (GLCNAC
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---- Local Similarity
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O00310;

O1-OCT-1994 (Rel. 30, Created)

O1-OCT-1994 (Rel. 30, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation updat
                                                                             Brown P.K., Romana L.K., Reeves P.R.;
"Molecular analysis of the rfb gene cluster
muenchen (strain_M67): the genetic basis of
                                                               groups C2 and B."
                                                                                                                                                                                                    Salmonella cholerae-suis (Salmonella enterica)
Bacteria; Proteobacteria; gamma subdivision; En
                                                                                                                                                                                                                                                                                                             RFBK_SALCH
                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                         Salmonella
                                                                                                                    MEDLINE=92349966; PubMed=1379320;
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         Microbiol. 6:1385-1394(1992).

FUNCTION: INVOLVED IN GDP-MANNOSE BIOSYNTHESIS WHICH SERVES AS THE ACTIVATED SUGAR NUCLEOTIDE PRECURSOR FOR MANNOSE RESIDUES IN CELL SURFACE POLYSACCHARIDES. THIS ENZYME PARTICIPATES IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LANNGKF-EFIAEEFQWNTVKQNGKSGACKRANVNDFFR-RLNWLTKSDGNAYPLQNLTK 181
                                                                                                                                                                                                                                                                                                                                                                              CDNNCI ---
                                                                                                                                                                                                                                                                                                                                                                                                         CNDFMFLGTEAISLGRVGDDFWCTDPSGDPNGTFWLQGCHMVHCAND-SLWM
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVKIDV----IHLLEMLCEDYGGRVDLAKAYYKAMTKSI-----NKHFKGNGVIASMEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---FRTSIQPGD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PVSVGCFVGFDASEPDSRHVVSIGK---LKDIRFMSIFRFKVWWTTHWVGR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGALGSPGCDHLNGAEWDVFIERPTAVD-----TCYPFDVPD------YQSIRSI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NGGSNVVSFDGLND-----MSSPFAIDGSDFTVNGHSFLSDVPENIVASPSPYTSIDKS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -- IDGWYGFR-HQNAEGTGTAADLKSTQAAIDQINGKLNRL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LKFQENYKFRDYVNPKATGPRAGQKGMKAFIDELKGEFKTVEHYYVWHALCGYWGGLRPQ
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Pred. No. 2;
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                                                                              of Salmonella
the polymorph
                                                                                                                                                                                                     Enterobacteriaceae;
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Best Local S
Matches 59
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Pfam; PF02880;
PROSITE; PS0071
                                                                                                                                                                                                                                                                                            VG64_HSVI1
Q00156;
Q1-DEC-1992
Q1-DEC-1992
Q1-DEC-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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Pfam; PF02878; PGM_PMM_I; 1.
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-1- PATHWAY: GDP-MANNOSE BIOSYNTHESIS WITHIN THE O ANTIGEN BIOSYNTHESIS PATHWAY OF LIPOPOLYSACCHARIDE BIOSYNTHESIS. -1- SIMILARITY: BELONGS TO THE PHOSPHOHEXOSE MUTASES FAMILY.
Davison A.J.;
"Channel catfish
                                                                       SEQUENCE FROM N.A. STRAIN-Auburn 1;
                                                                                                                                                                                             Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                     Hypotherical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACT_SITE
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                                                   MEDLINE-92087490;
                                                                                                                                            NCBI_TaxID=10401;
                                                                                                                                                                                                                       Ictalurid herpesvirus 1 (Channel catfish virus) (CCV).
                                                                                                                                                                           Ictalurid Herpes-like
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59; Conserv
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PGM_PMM_III; 1.
10; PGM_PMM; 1.
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                                                                                                                                                                                                                                                                     . 24, Created)
. 24, Last sequence up.
. 24, Last annotation of the control of th
                                                PubMed=1727613;
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FORMS THE PHOSPHOSERINE INTERMEDIATE
(BY SIMILARITY).

982E5B885083B893 CRC64;
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Best Local Similarity
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                                                                                                                                                       TRAL_HUMAN STANDARD; PRT; 712 AA. P51617; 01-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) Interleukin-1 receptor-associated kinase 1 (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SEQUENCE FROM N.A., AND PARTIAL SMEDLINE=96180673; PubMed=8599092. Cao Z., Henzel W.J., Gao X.;
                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                            Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein SEQUENCE 514 AA;
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                                                                     NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                         TELFWVIANI -- CT - FIFIHNKTIKLHH - GD -- - APDLNIDELPDGLYLFNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DYVNPKATGPRAGQKGMKAFIDELKGEFKTVEHVYVWHALCGYWGGLRPQVPGLPEARVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VKEAMKIVRTHLGTFRLLEEKTPPGIVDKFGWCTWDAFYLTVHPQGVIEGVRHLVDGGCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFRTSIQPGDDDFVDVCV-ESGSS-KVVDASFRSMLYLH-----AGDDP-----FAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KRLVDEGVLGMFRFNRMLTRVFFGYATGD-----DALIEGLLDTWFAFMVLLARFPVIPA 151
                                                                                                                                                                                                                                                                                                                                                                                                                                            -----HLEKVGI--DGV-----KIDVIHLLEMLCEDYGGRVDLAKAYYKAMTKSINKH 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGLVLIDDGWQSIGHDSDPITKEG------MNQTVAGEQMPCRLLKFQENYKFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -QLIDSNFCVLCMYESDHSLATADTRFKTILCDHFTEASVTAGGDPCDSAEVTAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -AVKRDTTLTTRKNGSINNFTKALNRARETCAMDRMESSLVEFQKKLREV
                                                                                       Chordata;
Primates;
                                    AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58198 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 101; DB Pred. No. 2.3;
                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88E7302A1424D29C CRC64;
                                                                                                                                                             2.7.1.-) (IRAK-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 172;
                                                                                                                                                                                                                                                                                                                                                                            491
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Best Local
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BINDING
ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                           Prodom; PD000001; PROSITE; PS00107;
                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00069; Pfam; PF00531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U52112; AAC51752.1; -. EMBL; AF030876; AAC08756.1; -. EMBL; AF031075; AAF21636.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L76191; AAC41949.1; EMBL; U52112; AAC51752.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted -!- FUNCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "IRAK: a kinase associated with the interleukin-1 receptor."; Science 271:1128-1131(1996).
[2]
                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                     Transferase;
                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genew; HGNC:6112; IRAK1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PTM: AN EXTENSIVE PHOSPHORYLATION OF ASSOCIATION WITH IL1-R-1. THIS STEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAR-1995) to the
                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                              116
                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
289
                                                       235
                                                                                    174
                                                                                                                 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEPENDENT: TISSUE SPECIFICITY: SEEMS TO BE UBIQUITOUS, ALTHOUGH PRESENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chwald K., Kioschis P., Rosenthal A., Platzer M.;
mitted (CCT-1997) to the EMBL/GenBank/DDBJ databases.
FUNCTION: INVOLVED IN IL-1 PATHWAY. THIS KINASE ASSOCIATES WITH
THE IL-1 RECEPTOR IL1-R-1. THIS ASSOCIATION IS RAPID AND IL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTIVATION OF THE KINASE.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMALL AMOUNTS
                                                                                    LYL----HAGDDPFALVKEAMKIVRTHLGTFRLLEEKTPPGIVDKFGWCTWDAFYLTVH
                                                                                                                                           ETQIVILEKSDSGRPYVFLLPIVEGPFRTSIQPGDDDFVDVCV--ESGSSKVVDASFRSM 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300283;
GFLPNGSLEDRLHCQTQACPP
                         ---PQGVIEGVRHLVDGGCPP 246
                                                       VYAVKRLKENADLEWTAVKQSFLTEVEQLSRFR-
                                                                                                               ESSYSLLQ----GARPFPFCWPLCE-----ISRGTHNFSEELKIGEGGFGCVYRAVMRNT
                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR000719; Euk_pkinase.
IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR000488; Death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBFAMILY.
                                                                                                                                                                                                                                  712
                                                                                                                                                                                                                                             212 521 PROTEIN KINASE; ATP-binding.
212 521 PROTEIN KINASE.
218 226 ATP (BY SIMILARITY).
229 ATP (BY SIMILARITY).
239 338 BY SIMILARITY.
196 196 F -> S (IN REF. 1).
532 532 S -> L (IN REF. 1).
                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                          death; ]
                                                                                                                                                                                                                                                                                                                                                                                                                       pkinase;
                                                                                                                                                                                                                                                                                                                                                                            PROTEIN_KINASE_ATP;
                                                                                                                                                                                                                                                                                                                                                                                        Euk_pkinase;
                                                                                                                                                                                                                                 76536 MW;
                                                                                                                                                                                        2.48;
27.08;
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to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                         17;
                                                                                                                                                                                        Score 100.5;
Pred. No. 4.1;
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                                                                                                                                                                         Mismatches
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COULD
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                                                           HPNIVDFAGYCAQNGFYCLVY
                                                                                                                                                                       61;
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BE LINKED TO
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- outstation
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RESULT 9
GLTB_SYNY3
ID GLTB_SYNY3

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Best Local
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-I- CATALYTIC ACTIVITY: 2 L-glutamate + 2 oxidized ferredoxin - L-glutamine + 2 reduced ferredoxin.
                                                                                                                                                                                                   METAL
METAL
SEQUENCE
                                                                                                                                                                                                                                             NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Existence of two ferredoxin glutamate synthases in to
'Existence of two ferredoxin glutamate synthases in to
cyanobacterium Synechocystis sp. PCC 6803. Isolation
inactivation of gltB and gltS genes.";
Plant Mol. Biol. 27:753-767(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for the requires a license agreement.
                                                                                                                                                                                                                                                                                                                Pfam; PF01493; DUF14; 1.
Pfam; PF01645; Glu_synthase;
                                                                                                                                                                                                                                                                                                                                                                     EMBL; X80485; CAA56652.1; -. EMBL; D90902; BAA17018.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                      entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95244836; PubMed=7727752;
Navarro F., Chavez S., Candau P.,
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                                                                                                                                                                                                                                                                                                       Oxidoreductase;
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                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002489; DUF14.
InterPro; IPR002932; Glu_synthase.
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  218
                               452
                                                          176
                                                                                     406
                                                                                                               120 VILEKSDSGRPYVFLLPIVEGPFRTS----IQPGDDDFVDVCVESGSSKVVDASFRSMLY 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: TO OTHER GLUTAMATE SYNTHASE CAUTION: IT IS UNCERTAIN WHETHER MET-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PATHWAY: GLUTAMINE SYNTHETASE/GOGAT PATHWAY IN THE ASSIMILATION OF AMMONIA. SYNTHASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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CTWDAFYLTVHPQGVIEGVRHLVDGGCPPGLVLIDDG:
                                                                                     LVIMASEAG ----- VLPI -- EPERVAKKGRLQPGRMFLVD -- MEQGRI - IADEEIK ---- 451
                                                       LHAGDDPFALVKEAMKIVRTH-----LGTFRLLEEKTPPGIVD-----KFGW
                                                                                                                                            al Similarity
136; Conserv
                                                                                                                                                                                                                                                                                     ctase; Iron-sulfur; 3Fe-4S; Flavoprotein; FAD;
blosynthesis; Complete proteome.
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                             ---QEIVSQHPYGEWLAANLKSLEQLPSPGNVPGTDAESLRQRQMAFGY
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                                                                                                                                                        19.98;
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                                                                                                                                                                                                    169071
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                                                                                                                                                                                       FMN (BY SIMILARITY).

FMN (BY SIMILARITY).

IRON-SULFUR (3FE-4S) (BY SIMILARITY).

IRON-SULFUR (3FE-4S) (BY SIMILARITY).

IRON-SULFUR (3FE-4S) (BY SIMILARITY).
                                                                                                                                       Pred. No. 14;
9; Mismatches
                                                                                                                                                           Score 100;
Pred. No.
                                                                                                                                                                                                                                                                       GLUTAMINE AMIDOTRANSFERASE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synechocystis
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                                                                                                                                                                     Length 1550;
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RESULT 10
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P52981;
01-0CT-1996 (Rel. 3
01-0CT-1996 (Rel. 3
15-JUN-2002 (Rel. 4
                                                                                                                                                                              Sugiura M., Tabata S.;
Sugiura M., Tabata S.;
"Sequence analysis of the genome of the unicellular cya
"Sequence analysis of the genome features
Synechocystis sp. strain PCC6803. I. Sequence features
Synechocystis sp. strain PCC6803. I. Sequence features
Synechocystis sp. strain PCC6803. I. Sequence features
                                                                                                                                                                                                                                                                                                                                                            GLGB
                                                This
                                                                                                                                                                                                                                                                                                          Synechocystis sp. (strain Bacteria; Cyanobacteria; Cyanobacteria; CRBI_TaxID=1148;
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                                                                                                                                                                      region from map positions 64\% to DNA Res. 2:153-166(1995).
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A MEDLINE-96127529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYNY3
                                between
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                                                                                   glycogen.

PATHWAY: Glycogen biosynthesis; third step.
SUBUNIT: MONOMER (BY SIMILARITY).

SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSY
                 European Bioinformatics Institute.
                                                                             KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                       CATALYTIC ACTIVITY:
              SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --LYLYQAKKLIL----SKPSQ
                                                                                                                                                                                                                                                                                                                                                            OR SLL0158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TSLYLSQAKEIQIKMAQGAKPGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LRSEYYAL - - - - - - PTRDCL - FED - - - - PLHNGETMLK IWNLNKF - TGVIGAFNCQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DFMFLGTEAISLGR-VGDDFWCTDPSGDPNGTFWLQGCHMVHCANDSLWMGNFIHPDWDM 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HLEKVGIDGVKIDVIHLLEMLCEDYGGRVDLAKAYYKAMTKSINKHFKGNGVIASMEHCN 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FDPNQGEAGLKTALDNLFTEADQAISQGANLIILSDRQVSAEKAAI-PALLAVSGLHHHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TKE---GMNQTVAGE-----QMPCRL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSISKEAHESLAIAM - - NRIGGKSNTGEGGEDPERFTWTNDQGDSKNSAIKQVASGRFGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -TFEELRILLAPMG-RDGVEAIGSMGADTPLAVLSDKPKLLYNYFQQLFAQVTNPPIDSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GLRPQVPGLPEARVIQPVLSPGLQMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHA
non-profit
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34, Last
41, Last
                                                                                                                                                                                                                                             PubMed=8590279;
A., Sato S., Kotani H.,
                                                                                                                                                                                                                                                                                                                                            (strain
 institutions
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Last annotation updat
ching enzyme (EC 2.4.1
                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                    Formation of 1,6-glucosidic
                                                                                                                                                                                                                                                                                                                              Chroococcales;
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2.4.1.18) (Glycogen branching
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-!- SIMILARITY: SOME SIMILARITY WITH

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Best Local
                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                            CYG1_CAEEL Q09435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PFC
Glycogen
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases -!- CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP + diphosper -!- SUBCELLULAR LOCATION: Type I membrane protein (Pote
                                                                                               Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                     Caenorhabditis elegans
                                                                                                                                   Guanylate cyclase receptor-type GCY-1 OR AH6.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACT_SITE
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ACT_SITE
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                                                 STRAIN-Bristol
                                                              SEQUENCE FROM
                                                                                   NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                      Jassal B.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKTPPGIVDKFGWCTWDAFYLTVHPQ--GVIEGVRHLVDGGCPPGLVLIDDGWQSIGHDS 262
                                                                                                                                                                                                                                                                                                                                                               GGRENLEAADFLRQVNSVVYSYFP
                                                                                                                                                                                                                                                                                                                                                                                     GGRVDLAKA-YYKAMTKSINKHFKGNGVIASMEHCNDF-----MFLGTEAISL----GR
                                                                                                                                                                                                                                                                                                                                                                                                             KEWGTLIFNYGRNEVRNFLVANALFWFDKYHIDGMRVDAVASMLYLDYCREEGEWVANEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPGLQMTMEDLA--VDKIVLHKVGL----VPPEKAEE-----MYEGLHAH-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EKTDP----YG-----FYQEVRPKTASIVADL------DGYQWHDEDWLEARRTS
                                                                                                                                  OR AH6.1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF02922; isoamylase_N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00128; alpha-amylase;
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77; Conserv
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554
770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -LVDKLIPYVKELGYTHIELLPIAEHPFDGSWG---YQVTGYYAPTSRFGSP--
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                                                N.A.
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486 E
554 E
89527 MW;
                                                                                               Nematoda; Chromadorea; cinae; Caenorhabditis.
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18.0%;
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l precursor
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                                                                                                                                                                                                         A
                                                                                                          Rhabditida; Rhabditoidea;
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n (Potential)
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CARBOHYD
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pfam; pF01094; ANF_receptor; 1.
proDom; pF000001; Euk_pkinase; 1
smART; SM00044; CYCc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z48009; CAA88089.1; -.
EMBL; Z48007; CAA88054.1; -.
EMBL; Z48009; CAA88054.1; JO
HSSP; Q02846; 1AWL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00069; pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WormPep; AH6.1;
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                    245
                                            735
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SIMILARITY: BELONGS TO ADI
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TDIHDVNPALIALVKDCWAEVPED
                                                                                      HKTFLRLHGNLRSATCLVNDSWQVKLAEYGMDNLVEEQTPPKKRLLWVAPEVLRGSLSVS
                                                                                                           FRSMLYLHAG-DDPFALVKEAMKIVRTHLGTFRLLEEKTPPG---
                                                                                                                                                       GGDLESETQIVILEKSDSGRPYVFLLPIVEGPFRTSIQPGDDDFVDVCVESGSSKVVDAS
                                                                                                                                                                             KERFVKMRKLDHENINRFIGLSI---DSAHFISVTKL-
                                                                                                                                                                                                                                             APSFKNGGSNVVSFDGLNDMSSPFAIDGSDFTVNGHSFLSDVPENIVASPSPYTSIDKSP
                                            QMEPSADIYSFAIIASEILTKKEAWDILD-
                                                                                                                                  RGSLQD-----ILSRGNFSMDYFFMF----
                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00452; GUANYLATE_CYCLASES_1;
PS50125; GUANYLATE_CYCLASES_2;
PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane;
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                    PPGLVLIDDGWQSIGHDSDPITKEGMNQTVAGEQMPCRLLKFQENYKFRDYVN
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Bourilss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,
RA Chim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinols S., Mauel C., Medigue C.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Parro V., Forman E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sekiguchi M., Tamakoshi A., Tanaka T., Tarahashi H., Takamaru K.,
Vasumoto Y., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Walta R., Yanamoto H., Yanane K., Yasumoto K., Yata K.,
Takelilla F., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
Tachtillus T., Wedler E., Wedler H., Weltzenegger T.,
Takelilla B., Rapotos S., Vandenoc K., Yata K.,
Takelilla R., Vandence G., Yata K.,
Takelilla R., Vandence G., Yata K.,
Takelilla R., Vandence K., Yasumoto K., Yata K.,
Takelilla R., Takelilla R., Takelilla R., Takelilla R
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                          "The complete genome subtilis.";
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(Rel. 38, Last sequence up
(Rel. 41, Last annotation
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Best Local
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SEQUENCE OF
STRAIN=168;
                                                                                                                                                                                                                                                 PIPA_DROME P13217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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             SEQUENCE FROM N.A.
MEDLINE-88311074; PubMed-2457447;
Bloomquist B.T., Shortridge R.D.,
Montell C., Steller H., Rubin G.,
                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
                                                                                                                                                                    01-JAN-1990 (Rel. 13, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase
(EC 3.1.4.11) (Phosphoinositide-specific phospholipase C)
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                                                                                                                                                              NORPA.
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                                                                                     NCBI_TaxID=7227
                                                                                                    Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein; Transferase; Kinase;
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306 AA;
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 phospholipase
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Pred. No. 1
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               Schneuwly Pak W.L.;
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gene
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of Drosophila,
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                              Perdew M.H.,
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L outstation -
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Best Local
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InterPro; IPR001192; F
InterPro; IPR000909; F
InterPro; IPR001711; F
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or send a
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                                                                                                                                                                                                                                                                                                                                                                ACT_SITE
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Prodom; PD001202; PI PLC_Y; 1
SMART; SM001239; C2; 1.
SMART; SM00148; PLCXC; 1.
SMART; SM00149; PLCYC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50004; C2_DOMAIN_2; 1.
PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. entities requires a license agreement (See )
                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                          444
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                                                                                                                                                                                                                                                                                                 Local Si
hes 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            its role in phototransduction.";

1 54:723-733(1988).

1 94:723-733(1988).

FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES DIACYLGLYCEROL (DAG) AND INOSITOL 1.4.5-TRISPHOSPHATE (IP3) IS MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPZ CENZYMES. NORPA IS INVOLVED IN PHOTOTRANSDUCTION.

CATALYTIC ACTIVITY: 1-phosphattdy1-1D-myo-inositol 4.5-bisphosphate + H(2)0 = D-myo-inositol 1.4.5-trisphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s SWISS-PROT entry is copyright. It is produced through a collab
ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diacylglycerol.
SIMILARITY: DON
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 VGLVP
                         -PDRPLDPGLPLPPPCKLKRKILIKNKRMKPE--
                                                   GGLRPQVPGL---PEARVIQPVLSPGLQMTMEDLAVDKIVLH---
                                                                              DCAFVSSEYPVILSFENHCN-----RAQQYKLAKYCDDFFGDLLLKEPL
                                                                                                          PCRLL--
                                                                                                                                SSVEMYRQTLLAGC---RCVELDCWNGKGEDEEPIVTHGHAYCTEILFKDCIQAIA----
                                                                                                                                                           GVIEGVRHLVDGGCPPGLVLIDDGWQSIGHDSDPITKEG-----
                                                                                                                                                                                        MSLDGFKRYLMSDENAPVFLDRLD-----
                                                                                                                                                                                                                THLGTFR--LLEEKTPPGIVDKFGWCTWDAFYL------
                                                                                                                                                                                                                                         TSITKGKQDFISLEQFIQFMNDKQRDPRMNEILYPLYEEKRCTEIINDYELDEEKKKNVQ
                                                                                                                                                                                                                                                                    TSIQPGDDDFVDV--CVESGSSKVVDASFRSMLY-LHAGD-----DPFALVKEAMKIVR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00168; C2; 1.
PF00387; PI-PLC-Y; 1.
PF00388; PI-PLC-X; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P10688;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  equires a license agreement (Semail to license@isb-sib.ch).
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673
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381
1095
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                                                                                                                                                                                                                                                                                                                                                                                                                                  degradation; Vision;
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PI_PLC.Xdom.
PI_PLC_Y.
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PEKAEEMYEGLHAHLEKVGIDGVKIDVIHLLEMLCEDYGG
                                                                                                                                                                                                                                                                                                 69;
                                                                                                                                                                                                                                                                                               Score 97.5; DI
Pred. No. 13;
59; Mismatches
                                                                                                                                                                                                                                                                                                                                                       W.
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C2 DOMAIN.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                      -FYMEMDQPLAHYYINSSHNTYLSGRQIGGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
                          VEKVELELWLKGELKTDDDPEEDAS
                                                                                                                                                                                                                                                                                                                         DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Hydroxymethylglutaryl-CoA synthase, cytoplasmic
synthase) (3-hydroxy-3-methylglutaryl coenzyme
                                                                                 PIR;
                                                                                                                          EMBL;
                                                                                                                                                EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gil G., Goldstein J.L., Slaughter C.A., Brown M.S.;

"Cytoplasmic 3-hydroxy-3-methylglutaryl coenzyme A synthase from the synthase from th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HMCS_CRIGR P13704;
                                                                                                                                                                                                                                                                                                                                      entities requires or send an email t
                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                 the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cricetulus griseus (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _CRIGR
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                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10029;
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                                                                                                                                                                                                                                                                                                                                                                                                     ween the Swiss Institute of Bioinformatics
European Bioinformatics Institute. There a
by non-profit institutions as long as
                                                                                                                     L; L00334; AAA37076.1; -.
L; L00326; AAA37076.1; JOINED.
L; L00327; AAA37076.1; JOINED.
L; L00328; AAA37076.1; JOINED.
L; L00329; AAA37076.1; JOINED.
L; L00330; AAA37076.1; JOINED.
L; L00331; AAA37076.1; JOINED.
L; L00332; AAA37076.1; JOINED.
L; L00332; AAA37076.1; JOINED.
L; L00332; AAA37076.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYNTHESIS OF STEROLS SUCH AS CHOLESTEROL SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE HMG-COA SYNTHASE FAMILY.
                                                                            ; L00333; AAA37076.1;
A25332; A25332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through
Pro: IPR000590; HMG_COA_SYNT.
PF01154; HMG_COA_SYNT; 1.
TE: PS01226; HMG_COA_SYNTHASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEDPFVFRKVVLPDLAVLRFGVY 760
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                                                                                                                                                                                                                                                                                                                                 equires a license agreement (S email to license@isb-sib.ch).
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Rodentia;
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Sciurognathi; Muridae; Cricetinae;
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cytoplasmic
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A synthase)
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p1-AUG-1990 (Rel. 15, Last sequence update)
01-AUG-1990 (Rel. 34, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
p1-CCT-1996 (Rel. 15, CHMG-18, Springer)
p1-CCT-1996 (Rel. 15, Last sequence update)
p1-CCT-1996 (Rel. 15, Last sequen
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ACT_SITE 129 129 POTENTIAL.
SEQUENCE 520 AA; 57318 MW; 2D4CAAE7DEE5D6RH CR
                                               Ayte J., Gil-Gomez G., Hegardt F.G.;

"Nucleotide sequence of a rat liver IDNA encoding the cytosolic 3-hydroxy-3-methylglutaryl coenzyme A synthase.";

Nucleic Acids Res. 18:3642-3642(1990).

-I- FUNCTION: THIS ENZYME CONDENSES ACETYL-COA WITH ACETOACETYL-COA TO FORM HMG-COA, WHICH IS THE SUBSTRATE FOR HMG-COA REDUCTASE.

-I- CATALYTIC ACTIVITY: (S)-3-hydroxy-3-methylglutaryl-COA + COA - acetyl-COA + H(2)O + acetoacetyl-COA.

-I- PATHWAY: PRODUCTION OF MEVALONATE FROM HMG-COA PRIOR TO THE SYNTHESIS OF STEROLS SUCH AS CHOLESTEROL AND ISOPRENOIDS.

-I- SUBCELLULAR LOCATION: Cytoplasmic.

-I- SIMILARITY: BELONGS TO THE HMG-COA SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Sprague-Dawley; TISSUE-Liver; MEDLINE-90301491; PubMed-1972979;
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Pfam; PF01154; HMG_CoA_synt; 1.
PROSITE; PS01226; HMG_COA_SYNTHASE; 1.
Lyase; Cholesterol biosynthesis; Multigene family.
ACT_SITE 129 129 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                   HEAPIGLVNMLNTSGAIQSVDYDDDLSSVEIGVKGCGEMRVFASKKPRACRIDGEDVGFK
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Maximum DB
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  Score
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length: 2000000000
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1: /cgn2_6/ptodata/1

2: /cgn2_6/ptodata/1

3: /cgn2_6/ptodata/1

4: /cgn2_6/ptodata/1

5: /cgn2_6/ptodata/1

6: /cgn2_6/ptodata/1
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                      GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
/cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/1/1aa/6CTUS_COMB.pep:*
/cgn2_6/ptodata/1/1aa/backfiles1.pep:*
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US-09-819-993-2

US-09-819-993-5

US-08-305-505-6

US-08-717-515-8

US-08-525-654A-1

US-08-525-654A-1

US-09-004-838-131

US-09-004-838-131

US-09-004-838-133

US-09-004-838-133

US-09-004-838-103

US-09-094-838-103

US-09-134-078-28

US-09-134-078-28
                                                                                                                                                                   US-09-004-838-101
US-09-004-838-47
US-08-040-751-3
US-08-291-368-2
US-08-962-190-2
PCT-US-5-10310-2
5164180-4
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US-08-846-234-1
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US-09-298-924-6	US-09-242-690A-15	US-09-004-838-108	US-09-423-468A-15	US-09-134-001C-2980	US-09-313-677-17	US-09-313-677-19	US-09-313-677-2	US-09-313-677-21	US-09-066-047-5	US-08-403-853-10	US-08-810-712-10	US-09-423-468A-13	US-08-687-580B-7	US-09-364-970-8	US-09-388-743-22	PCT-US96-09193-2	US-09-307-185-5
6, A	Sequence 15, Appl	Sequence 108, App	Sequence 15, Appl	Sequence 2980, Ap	Sequence 17, Appl	Sequence 19, Appl	Sequence 2, Appli	Sequence 21, Appl	Sequence 5, Appli	Sequence 10, Appl	Sequence 10, Appl	Sequence 13, Appl	Sequence 7, Appli	Sequence 8, Appli	Sequence 22, Appl		Sequence 5, Appl1

LIGNMENTS

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TYPE: amino a TOPOLOGY: lir MOLECULE TYPE: US-08-846-234-5
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US-08-846-234-5
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PAtentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION NUMBER: US/08/846,234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08846234 Patent No. 6166292
                                                                                                                                               Query Match 100.0%; Score 4225; Best Local Similarity 100.0%; Pred. No. 0; Matches 784; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                       TELEFAX: (703) -415 --- 5:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
SEQUENCE TRANSPORTED STATES
1.ENGTH: 784 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: NOZAKI Jinshi
APPLICANT: KIDA Takao
TITLE OF INVENTION: RAFFINOSE SYNTHASE GENE,
TITLE OF INVENTION: PRODUCING RAFFINOSE, AND
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                      61
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                                                                                1 MAPSEKNGGSNVVSFDGLNDMSSPFAIDGSDETVNGHSFLSDVPENIVASPSPYTSIDKS 60
                      PVSVGCFVGFDASEPDSRHVVSIGKLKDIRFMSIFRFKVWWTTHWVGRNGGDLESETQIV 120
                                                              MAPSFKNGGSNVVSFDGLNDMSSPFAIDGSDFTVNGHSFLSDVPENIVASPSPYTSIDKS
amino acid
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(703)-413-2220
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TRANSGENIC PLANT
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                                                                                                                                                                                                                                                                 Sequence 1, Application US/08846234 Patent No. 6166292
                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                           TITLE OF INVENTION: RAFFINOSE SYNTHASE GENE, TITLE OF INVENTION: PRODUCING RAFFINOSE, AND NUMBER OF SEQUENCES: 22
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
OPERATING SYSTEM: PC-DOS,
                                                                                                                                                                                                      APPLICANT: OSUMI Chieko
APPLICANT: NOZAKI Jinshi
APPLICANT: KIDA Takao
                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                          781
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                                                                                    STREET: 1755 S. CITY: ARLINGTON STATE: VIRGINIA
                                                          COUNTRY: UZIP: 22202
                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDPNGTFWLQGCHMVHCANDSLWMGNFIHPDWDMFQSTHPCAAFHAASRAISGGPIYVSD 540
                                                                                                                                                                                                                                                                                                                                                          EYLF 784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGRVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLGTEAISLGRVGDDFWCTDPS
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                                                                                                                   E: OBLON,
1755 S. JI
                                                                        USA
                                                                                                                N, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
Compatible
PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                   TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (703)-413-22: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600
FILING DATE: 21-DC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gonsalves, Dennis
APPLICANT: Ling, Kai-Shu
APPLICANT: Ling, Kai-Shu
TITLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS PROTEINS AND
TITLE OF INVENTION: THEIR USES

TITLE OF SEQUENCES: 32
                                                                                                                                                          REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,544
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
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                                  TYPE: amino STRANDEDNESS:
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ZIP: 14603
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STATE: New York
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Y: U.S.A.
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GY: linear
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APPLICANT: Kramer, Vance C.
APPLICANT: Morgan, Michael K.
APPLICANT: Morgan, Arne R.
APPLICANT: Hart, Hope
APPLICANT: Hart, Hope
APPLICANT: Warren, Gregory W.
APPLICANT: Dunn, Martha
APPLICANT: Dunn, Martha
APPLICANT: Chen, Jeng S.
TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
TITLE OF INVENTION: AND NUCLEIC ACID SEQUENCES CODING THEREFOR
FILE REFERENCE: CGC1963/A
CURRENT APPLICATION NUMBER: US/09/251,645
CURRENT FILING DATE: 1999-02-17
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                          Sequence 6, Application US/09251645 Patent No. 6281413 GENERAL INFORMATION:
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Best Local
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; TYPE: PRT
; ORCANISM: Photorhabdus luminescens
US-09-251-645-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            502 NKIARTFSYVNSP-TSKSHGSLAKITSVMNNQQTVTTFKYEYSESEMTTNATVTGFDG--
                                                               684 --VSPVTKLIQTSLHFAPIGLV---NMLNTSGAIQSVDYDDDLSS-VEIGVKGCGEMRVF 737
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TLLSASEGVSQTNYSYFPSGVLQRESFLRDNKPISSGEYLYTMSGLIQRHKDSFGHNHVY
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                                                                                                                                      -VGGRKTEYLYGPQGDKPIQSITPSHNKQNMDYLYYLGSVMSKFTTGTDQQNFRYHSKTG
                                                                                                                                                                                                                                                                                                                                                                                                                                  HAT-----QIGYDVFDRIVKKTLPDGTILESAYASF-----SHEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----LWMGNE------THPDWDMFQS-----THPCAAF 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1584;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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738 ---ASKKPRACRIDGEDVGFKYDQDQMVVVQVPWPIDSSSGGISVIEY 782

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                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 6350933
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Shen, Kathy
APPLICANT: Meyers, Blake
TITLE OF INVENTION: Procedures and Materials for
TITLE OF INVENTION: Conferring Pest Resistance in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 023070-078810US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/781,734 FILING DATE: 10-JAN-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
 406 KIDVIHLLEMLC---
                                                          165
                                                                                                                                    120
                                                                                                                                                                       291
                                                                                                                                                                                                                                             237 RHLVDGGCPPGLVLIDDGWQSIGHDS---DPITKEGMNQTV---AGEQMPCRLLKFQENY 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/OFILING DATE: 09-JAN-1998 CLASSIFICATION: 800
                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Einhorn, Grego
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Francisco
                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                        GLPIAIKTIALSLKGRSKSAWDVALSRLENHKIG--SEEVVREVF-----KISYDNL 214
                                                                                             GLPEARVIQPVLSPGLQMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGIDGV 405
                                                                                                                                  ---SILNIKVLKDVEGQSLFRQFAKNAGDDDLDPAFN--
                                                                                                                                                                   KFRDYVNPKATGPRAGQKGMKAFI-----DELKGEFKTVEHVYVWHALCGYWGGLRPQVP 345
                                                                                                                                                                                                          RFEADGGKNKFLVILDDVWQFVDLEDIGLSPLPNKGVNFKVLLTSRDSHVCTLMGAEAN- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101, Application US/09004838
o. 6350933
                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                     1..487
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ED-----YGGRVDL---AKAYYKAMT------
                                                                                                                                                                                                                                                                                                     2.5%; Score 107; DB 4; 20.1%; Pred. No. 0.035;
                                                                                                                                                                                                                                                                                                                                                                             /note= "RG2G deduced sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101:
                                                                                                                                                                                                                                                                                  63; Mismatches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #
                                                                                                                                                                                                                                                                                                                       Length 487
                                                                                                                                                                                                                                                                                  Indels 124;
                                                                                                                              -GIADSIASRCQ 164
                   -KSIN 439
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US-09-004-838-47
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               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 47, Application US/09004838 Patent No. 6350933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                               TELEFAX: (415) 576-03
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF THE PROPERTY ADDRESS:

CORRESPONDENCE ADDRESS:

Townsend and Townsend and Crew LLP

ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                    FEATURE:
                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Procedures
TITLE OF INVENTION: Conferring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     372
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                                                                                          LOCATION: 1..488
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/781,734 FILING DATE: 10-JAN-1997
                                                                                                                               NAME/KEY:
                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                      STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                      NAME: Einhorn, Gregory P. REGISTRATION NUMBER: 38,440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                            LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KHFKGN--GVIASMEHCNDF---MFLGTEAISLGRVGDDFWCTDPSGDPNGTFWLQGCHM
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                                                                                                                                                                                                                         amino acid
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                                                                                                                                                                                                                                           488 amino acids
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                                                                                                                                                                                                                                                                                                (415) 576-0300
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                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                    (415)
                                                                                                                                                                 protein
                   2.5%;
                                                                                                                                                                                                                                                                                                                    576-0200
                                                                                          /note= "RLG2G protein"
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                                                                                                                                                                                                                                                                                                                                                        023070-078810US
Score 107; DB 4; Length 488; Pred. No. 0.035; Mismatches 167; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and Materials for Pest Resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Version #1.30
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Matches

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Conservative

63;

Indels 124;

Gaps

21;

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US-08-040-751-3
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Patent No. 5407825
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                      SOFTWARE: PATEHLATION DATA:
CURRENT APPLICATION NUMBER: US/
APPLICATION NUMBER: 1930329
                                                                                                                                                                  FILING DATE: 19930329
CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: SALIWANCHIK, DAVID R.
REFERENCE_/DOCKET NUMBER: MA31
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Payne, Jewel M
APPLICANT: Sick, August J
TITLE OF INVENTION: No. 5407825el Bacillus thuringiensis isolates
TITLE OF INVENTION: active against Lepidopteran Pests and Genes En
TITLE OF INVENTION: Lepidopteran-active Toxins
                                                              SEQUENCE CHARACTERISTICS: LENGTH: 1174 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSE: DAVID R. SALIWANCHIK
ADDRESSEE: DAVID R. SALIWANCHIK
STREET: 2421 N.W. 41st STREET, SUITE A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         546
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                                     TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: GAINESVILLE
STATE: FL
                      STRANDEDNESS:
                                                                                                                                              TELEFAX: 904-372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                    single
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; LIBRARY: Lambd
; CLONE: 81A2
US-08-040-751-3
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Best Local Similarity
                                                                                                                                                                                                                                   GENERAL INFORMATION:
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HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
                                                                                           TITLE OF INVENTION: No. 5686069el Bacillus thuri
TITLE OF INVENTION: Active Against Lepidopteran
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                              APPLICANT: Payne, Jewel M.
APPLICANT: Sick, August J.
TITLE OF INVENTION: No. 5686069el Bacillus thuringiensis Isolates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                336 YWGGLR-----PQVPGLPE-----ARVIQPVLSPGLQMTMEDLA-----VDK 372
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INDIVIDUAL ISOLATE:
COUNTRY:
                      STATE:
                                          CITY: Gainesville
                                                         ADDRESSEE: Sallwanchik & Sallwanchik STREET: 2421 N.W. 41st Street, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                VKGCGEMRVFASKKPRACRIDGEDVG 753
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Pred. No. 0.
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                                                                                                                                                Pests
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ZIP: 32606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: PHYPOTHETICAL: YENANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1174 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA50.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904)375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07,
FILING DATE: 15-0CT-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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LIBRARY: La...
ONE: 81A2
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                   642 PISIEGV--KTFALYLYQAKKLILSK--
                                                                                                                                                                                                              546 TMSANGSLTSQSFRFAEFPVGIST-----SGSQTAG-ISISNNPGRQTFHLDRIEF
                                                                                                                                                                                                                                                 495 VHCANDSLWMGNFIHPDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLV 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 314 YWAGHRVTSHFTGSSQVISSPQYGITANAEPSRTIAPSTFPGLNLFYRTLSDPFFRRSDN 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Saliwanchik, David R. REGISTRATION NUMBER: 31,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: si
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                                                                                            WCRETRRNQCFS-QYSKRVTSKTN----
                                                                                                                                 IPVDATFEAEYDLERAQKAVNSLFTS---SNQIELKTDVTDYHIDQVSNLV---DCLSDE 649
                                                                                                                                                           LPDGSILRSEY---YALPTRDCLFEDPLHNGETMLKI----WNLNKFTGVIGAFNCQGGG
                                                                                                                                                                                                                                                                                         FTGGDIIRTNVNGNVLSMSLNFSNTSLQRYRVRVRYAASQTMVMRVNVGGSTTFDQGFPS
                                                                                                                                                                                                                                                                                                                              RVGDDFWCTDPSGD------
                                                       FCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDRGWRGSTDITIQGGDDVFKEN
                                                                                                                                                                                                                                                                                                                                                               SHVTLTRSLYNTNITSLPTFVWTHHSATDRNIIYPDVITQIPLVKSFSLTSGTSVVRGPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 181;
                                                                                                                                                                                                                                                                                                                            -----PNGTFWLQGCHM 494
                   -----PSQDLDIALDPF--EFELIT 683
Length 1174;
                                                                                            -PKDIEWHSG----EN 641
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; CLONE: 81A2
US-08-962-190-2
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US-08-962-190-2
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                                                     Best Local Similarity Matches 111; Conserv
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INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: MA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904)375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 15-OCT-90
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1174 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Sick, August J.
TITLE OF INVENTION: No. 5985267el Bacillus thuringiensis Isolates
TITLE OF INVENTION: Active Against Lepidopteran Pests
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HYPOTHETICAL: Y
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336 YWGGLR------PQVPGLPE------ARVIQPVLSPGLQMTMEDLA-----VDK 372
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                  STRAIN: aizawai
INDIVIDUAL ISOLATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 2421 N.W. CITY: Gainesville
                                                                                                                                                                                                                                 ORGANISM:
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                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                       Conservative
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                                                                                                                                                               Lambdagem -
                                                                                                                                                                                                                                     Bacillus thuringiensis
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                                                                     Score 107;
Pred. No. 0.
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                                                   Mismatches
                                                                                        DB 2;
                                                       181;
                                                                                        Length 1174;
                                                     Indels 192;
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RESULT 10
PCT-US95-10310-2
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                                                                                                      COUNTRY: US
COUNTRY: US
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION NUMBER: PCT/US95/10310
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: POSTAL CODE/ZIP: 92121

APPLICANT: PHONE NUMBER: (619) 453-8030

APPLICANT: FAX NUMBER: (619) 453-6991

TITLE OF INVENTION: Protein Toxins Active Against Lepidopteran Pests NUMBER OF SEQUENCES: 27

CORPERCONNECT: 27
              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07,
FILING DATE: 15-OCT-90
                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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CLASSIFICATION:
                                                                                                FILING DATE:
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CITY: San Diego
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LIBRARY: Lambd
CLONE: 81A2
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NAME: Saliwanchik, David R.
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STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MASO.C1
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INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM:
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                                                                                                                                                              V-GCTDLQ-
                                 VKGCGEMRVFASKKPRACRIDGEDVG 753
                                                                                                                                                                                                                                                     WCRETRRNQCFS-QYSKRVTSKTN---
                                                                                                                                                                                                                                                                                                                         LPDGSILRSEY---YALPTRDCLFEDPLHNGETMLKI----WNLNKFTGVIGAFNCQGGG 607
                                                                                                                                                                                                                                                                                                                                                                                             VHCANDSLWMGNFIHPDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLV 554
                                                                                                                                                                                                                                                                                                                                                                                                                                    FTGGDIIRTNVNGNVLSMSLNFSNTSLQRYRVRVRXAASQTMVMRVNVGGSTTFDQGFPS 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHVTLTRSLYNTNITSLPTFVWTHHSATDRNIIYPDVITQIPLVKSFSLTSGTSVVRGPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRVDLAKAYYKAMTKSI------NKHFKGNGVIASMEHCNDF-MFLGTEAI-SLG 468
                                                                                                     VSPVTKLIQTSLHFAPIGLVNMLNTSGAIQSVDYDDDLS------
                                                                                                                                         YVTLPGTFDECYPTYLYQ--KIDESKLKAYNRYQLRGYIEDSQDLEIYLIRYNAKHETVN 767
                                                                                                                                                                                                                 FCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDRGWRGSTDITTIQGGDDVFKEN 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RVGDDFWCTDPSGD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMPTLGINVVQGVGFIQPNNGEVLYRRRGTVDSLDELPIDGENSLVGYSHRL----- 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I-----VLHKVGLVPPEKAEEMY--EGLHAHLEKVGIDGVK--IDVIHLLEMLCEDYG 421
                                                                     VPGTGSLWPLSVE-SPIGRCGEPNR--CVPHLEWNPDLDCSCRDGEKCAHHSHHFSLDID 824
                                                                                                                                                                                                                                                                                       IPVDATFEAEYDLERAQKAVNSLFTS---SNQIELKTDVTDYHIDQVSNLV---DCLSDE 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1174 amino acids
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19.6%;
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 835
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                                                                                                                                                                                                                                                   ---PKDIEWHSG----EN 641
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29;

RESULT 11 5164180-4

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US-08-846-234-2; Sequence 2, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; SEQ ID NO:4:
                                                                                                                                                                            Sequence 2, Application US/08846234 Patent No. 6166292 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/451,389
FILING DATE: 14-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 353,860
FILING DATE: 18-MAY-1989
                                                                                                              APPLICANT: OSUMI Chieko
APPLICANT: NOZAKI Jinshi
APPLICANT: KIDA Takao
                                      CORRESPONDENCE ADDRESS
                                                       TITLE OF INVENTION: RAFFINOSE SYNTHASE GENE, TITLE OF INVENTION: PRODUCING RAFFINOSE, AND NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Payne, Junitable of INVENTION:
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                                                                                                                                                                                                                                                                                                                     825 V-GCTDLQ------EDLG 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   546 TMSANGSLTSQSFRFAEFPVGIST-----SGSQTAG-ISISNNPGRQTFHLDRIEF
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                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PISIEGV--KTFALYLYQAKKLILSK-----
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OBLON, SPIVAK,
55 S. JEFFERSON
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N: BACILLUS THURINGIENSIS ISOLATES ACTIVE
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MCCLELLAND, MAIER & NEUSTADT, DAVIS HIGHWAY, FOURTH FLOOR
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                                                                                                METHOD FOR
                                                                             TRANSGENIC
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                                                                                PLANT
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                                                                                                                                                                                                                                                                                                  ; ORGANISM: Human US-09-819-993-2
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                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application Patent No. 6436692 GENERAL INFORMATION:
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Best Local S
                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/819,993
CURRENT FILING DATE: 2001-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: GONG, Fangcheng et al.
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS,
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                  LENGTH: 478
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
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 525
                                  136
                                                                  465
                                                                                                                                  413
                                                                                                                                                                                                378 VGLVPPE-----KAE-EMYEGLHAHLEKVGIDGVKID------VIHL 412
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ZIP: 222
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nes 19; Conserv
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                  Local Similarity
les 77; Conserv
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                                    VF - -
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                                                                                                                                                                 VGIVALEIYFPSQYVDQAELEKYDGVDAGKYTIGLGQAKMGFCTDREDINSLCMTVVQNL 76
HAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALPTRDCLFEDPLHNGET
                                                               ISLGRVGDDFWCTDPSGDPNGTFWLQGCHMVHCANDSLWMGNFIHPDWDMFQSTHPCAAF 524
                                                                                                   MERNNLSYDCIGRLEVGTETIIDKSKSVKTNLMQLFEESGNTDIEGIDTTN-ACYGGTAA
                                                                                                                                  LEM -- LCEDYGGRVDLAKAYYKAMTKSINKHF-----KGNGVIASMEHCNDFMFLGTEA 464
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(703)-413-2220
OR SEQ ID NO: 2:
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100.0%; Pr
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Pred. No.
                                                                                                                                                                                                                                                Score 102; DB 4; Length 478; Pred. No. 0.11;
                                                                                                                                                                                                                                    Mismatches
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0.00018;
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                                                                                                                                                                                                                                    Indels 190;
                                  -SSWDGLRGTHM----
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GENERAL INFORMATION:
APPLICANT: GONG, FANGCheng et al.
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTE
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOO1195
CURRENT APPLICATION NUMBER: US/09/819,993
CURRENT FILING DATE: 2001-03-29
NUMBER: FOR SEQ ID NOS: 5
SOCTWARE: FRSTSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 518
TYPE: PRT
ORGANISM: Human
US-09-819-993-5
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US-09-819-993-5
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-EDTYFDRDVEK 317
                                                                GEDVGFKYDQDQ 760
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US-08-305-505-6
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INFORMATION FOR SEQ ID NO:
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FILING DATE: 02 JUNE 1993
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Jean C.
NAME: Baker, Jean C.
REGISTRATION NUMBER: 65-03
REFERENCE/DOCKET NUMBER: 65-05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 520 amino acids
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
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                             629 TNPKDIEWHSGENPISIEGVKTFALYLYQAKKLILSKPSQDLDIALDPFEFELITVSPVT
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                                                                                                                                               164 ATGNARPTGGVGAVALLIGPNAPLIFERGLRGTHMQHAYDFYK----PD----MLSEY---
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                                                                                                                                                                                                                                                                                                      77
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STATE: Wisconsi
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411 East Wisconsin Avenue
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SYNTHASE PREPARATION WITH IMPROVED
STABILITY
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; Pred. No. 0.22;
59; Mismatches 111; Indels 180;
-------QKEANDNDFTLNDFGF-MIFHSPYC
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                                                                                                                                                                                    ----KHNFDLLKKLVLPDGSILRSEYYAL 568
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                                                                      -CYLSALDRCYSVYCKKIHA- 242
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                                                                                                                                                                                                                            163
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20;

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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
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       Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa//S

2: /cgn2_6/ptodata/2/pubpaa//S

3: /cgn2_6/ptodata/2/pubpaa//S

4: /cgn2_6/ptodata/2/pubpaa//S

6: /cgn2_6/ptodata/2/pubpaa//S

6: /cgn2_6/ptodata/2/pubpaa//S

7: /cgn2_6/ptodata/2/pubpaa//S

8: /cgn2_6/ptodata/2/pubpaa//S

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10: /cgn2_6/ptodata/2/pubpaa//S

11: /cgn2_6/ptodata/2/pubpaa//S

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12: /cgn2_6/ptodata/2/pubpaa//S

13: /cgn2_6/ptodata/2/pubpaa//S

14: /cgn2_6/ptodata/2/pubpaa//S

15: /cgn2_6/ptodata/2/pubpaa//S

16: /cgn2_6/ptodata/2/pubpaa//S

17: /cgn2_6/ptodata/2/pubpaa//S

18: /cgn2_6/ptodata/2/pubpaa//S

19: /cgn2_6/ptodata/2/pubpaa//S

10: /cgn2_6/ptodata/2/pubpaa//S

11: /cgn2_6/ptodata/2/pubpaa//S
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4225
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: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep: *
: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep: *
: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep: *
: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep: *
: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19 1	17	16	15	14	13	12	11	10	9	œ	7	თ	σ	4	w	2	_	Result No.
91.5	91.5	92.5	93	94	95.5	95.5	95.5	95.5	95.5	96	96	96.5	98	100	101.5	102	106.5	Score
2.		2.2	2.2	2.2	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.4	2.4	2.4	2.5	Query Match
781	304	1356	26926	1021	712	712	712	712	344	772	520	862	1431	518	626	478	905	Length
9 1	10	9	9	9	10	10	10	10	10	9	9	9	12	9	12	9	10	BG
US-09-866-050A-668	US-09-970-638-4	US-10-077-111-10	US-09-759-508B-2	US-10-101-464A-954	US-09-771-161A-264	US-09-771-161A-263	US-09-771-161A-262	US-09-773-753-5	US-09-771-161A-173	US-10-121-032-28	US-10-193-295-4	US-09-978-522-1	US-10-095-718-4	US-10-193-295-5	US-10-001-851-27	US-10-193-295-2	US-09-728-721-52	ID
sequence 568, App	Sequence 4, Appl	Sequence 10, Appl	Sequence 2, Appli	~	Sequence 264, App	Sequence 263, Ap	Sequence 262, App	Sequence 5, Appli	73	Sequence 28, Appl	Sequence 4, Appli	Sequence 1, Appli	Sequence 4, Appl	Sequence 5, Appli	Sequence 27, App	Sequence 2, Appli	Sequence 52, App	Description

45	44	43	42	41	40	39	38	37	36	ω 5	34	ယ	32	31	30	29	28	27	26	25	24	23	22	21	
86.5	86.5	87	87	87	87	87.5	87.5	88.5	88.5	89	89	89.5	89.5	89.5	89.5	89.5	89.5	90	91	91	91	91	91	91	
2.0	2.0	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1						2.2		
561	559	11877	11877	625	325	1410	559	538	525	559	350	1786	1786	1725	1482	1212	559	595	3472	3472	3472	809	802	378	0
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US-09-925-301-1006	US-10-001-851-20	US-09-861-289-6	US-09-860-846-6	US-09-925-302-449	US-09-765-272-80	US-10-014-717-3	US-10-001-851-22	US-10-043-487-329	US-09-738-626-6109	US-09-908-855-15	US-09-738-626-4030	US-09-938-275-7	US-10-037-182-10	US-10-037-182-12	US-09-815-242-12484	US-09-815-242-5279	US-10-001-851-21	US-09-738-626-5826	US-10-027-801-4	US-10-034-623-4	US-10-027-806-4	US-10-080-114A-12	US-10-080-114A-2	US-09-816-664-7	***************************************
Sequence 1006, Ap	Sequence 20, Appl	Sequence 6, Appli	Sequence 6, Appli	Sequence 449, App	Sequence 80, Appl	Sequence 3, Appli	Sequence 22, Appl	Sequence 329, App	Sequence 6109, Ap	Sequence 15, Appl	Sequence 4030, Ap	Sequence 7, Appl1	Sequence 10, Appl	Sequence 12, Appl	Sequence 12484, A	Sequence 5279, Ap	Sequence 21, Appl	Sequence 5826, Ap	Sequence 4, Appli	۵.	Sequence 4, Appli	Sequence 12, Appl	Sequence 2, Appli	Sequence 7, Appli	the date of the board

ALIGNMENTS

Qy 2	Qy 2	Db 1	Quer Best Matc	RESULT 1 Sequence Sequence Patent GENERAL FITLE
256QSIGHDSDPTTKEGMNQTVAGEQMPCRLLKFQENYKFRDYVNPKA 300 : : : : : : :: : 195 EEPDDSLYLEEGEESLGYPED-VLEEGAGDDPQCFVYDSEEECEYEE 242	215 FGWCTWDAFYLTVHPQGVIEGVRHLVDGGCPPGLVLIDDGW 255	100 GTGEVVEVS-RGLEDPFSLGTITPEIAELSEEKECPGLGAPE 140	Query Match 2.5%; Score 106.5; DB 10; Length 905; Best Local Similarity 20.2%; Pred. No. 0.65; Matches 134; Conservative 90; Mismatches 203; Indels 235; Gaps 37;	WESULT 1 US-09-728-721-52 Sequence 52, Application US/09728721 Patent No. US20020061845A1 GENERAL INFORMATION: APPLICANT: Bertlin, John TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES TH FILE REFERENCE: 07334-124001 CURRENT APPLICATION NUMBER: US/09/728,721 CURRENT FILING DATE: 2000-12-01 PRIOR APPLICATION NUMBER: US/09/728,721 CURRENT FILING DATE: 1999-06-28 PRIOR APPLICATION NUMBER: US 09/207,359 PRIOR FILING DATE: 1998-12-08 PRIOR APPLICATION NUMBER: US 09/207,359 PRIOR APPLICATION

296 VROPYLSPGLOMTHE
GLHAHLEK
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	Qy 492 CH 493 Db 521 CH 522	
*	Qy 454CNDFMELGTEAISLGRVGDDFWCTDPSGDPNGTFWLQG 491	
	Qy 398 EKVGIDGVKIDVIHLLEMLCEDYGGRVDLAKAYYKAMTKSINKHEKGNGVIASMEH 453 : : :	
	Qy 368LAVDKIVLHKVG	
	Qy 325EHVYVMHALCGYWGGLRPQVPGLPEARVIQPVLSPGLQMTMED 367 :: :: :: : : : :	
	Qy 279 MPCRLLKFQENYKFRDYVNPKATGPRAGOKGMKAFIDELKGEFKTV 324	
	Qy 220 WDAFYLTVHPQGVIEGV-RHLVDGGCPPGLVLIDDGWQSIGHDSDPITKEGMNQTVAGEQ 278	
20;	Query Match 2.4%; Score 101.5; DB 12; Length 626; Best Local Similarity 21.3%; Pred. No. 1.1; Matches 77; Conservative 52; Mismatches 118; Indels 115; Gaps	
	NUMBEI SOFTWI SEQ ID LENGT TYPE ORGAN S-10-001	
	CURRE CURRE PRIOR	
Transfer	ICANT:	
	RESULT 3 US-10-001-851-27 ; Sequence 27, Application US/10001851	
	Qy 705 MLNTSGAIQSVDYDDDLSSVEIGVKGCGEMRVFASKKPRACRIDGEDVGFKYDQDQ 760	
	Db 203QKEGNDKDFTLNDFGF-MIFHSPYCKLVQXSLARMLLND 240	
	179 SIQCYLSALDRCYSVYCKKIHAQW	
	SRS MT KTUNTUKEMANTAAENOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO	
	Qy 525 HAASRAISGGPIYVSDSVGKHNEDLIKKLVLPDGSIIRSEYVALPTRDCLFEDPLHNGET 584 Db 157	
	36 VFSSWDGLRGTHM 1	

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; LENGTH: 518
; TYPE: PRT
; ORGANISM: Human
US-10-193-295-5
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TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
TITLE OF INVENTION: THERROF
FILE REFERENCE: CL001195DIV
CURRENT APPLICATION NUMBER: US/10/193,295
CURRENT FILING DATE: 2002-07-12
PRIOR APPLICATION NUMBER: 08/819,993
PRIOR APPLICATION NUMBER: 08/819,993
PRIOR APPLICATION NUMBER: 08/819,993
PRIOR FILING DATE: 2001-03-29
INUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
                                                                                                                                                                                US-10-055-718-4
US-10-095-718-4
; Sequence 4, Application US/10095718
; Patent No. US20020131956A1
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APPLICANT: Walsh, Christopher APPLICANT: Chao, Hengjun APPLICANT: Burstein, Haim APPLICANT: Lynch, Carmel APPLICANT: Stepan, Tony APPLICANT: Stepan, Tony APPLICANT: Munson, Keith TITLE OF INVENTION: Methods of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/10193295
Patent No. US20020173018A1
GENERAL INFORMATION:
APPLICANT: GONG, Fangcheng et al.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAASRAISGGPIYVSDSVG-------KHNFDLLKKLVLPDGSILRSEYYAL 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MERNNLSYDCIGRLEVGTETIIDKSKSVKTNLMQLFEESGNTDIEGIDTTN-ACYGGTAA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEM--LCEDYGGRVDLAKAYYKAMTKSINKHF-----KGNGVIASMEHCNDFMFLGTEA 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VGIVALEIYFPSQYVDQAELEKYDGVDAGKYTIGLGQAKMGFCTDREDINSLCMTVVQNL 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----W-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISLGRVGDDFWCTDPSGDPNGTFWLQGCHMVHCANDSLWMGNFIHPDWDMFQSTHPCAAF 524
                                                                                                                                                                                                                                                                                                         -EDTYFDRDVEK 317
                                                                                                                                                                                                                                                                                                                                                                                                                            KLIQTSLHFAPIGLVNMLNTSGAIQSVDYDDDLSSVEIGVKGCGEMRVFASKKPRACRID 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----CYLSALDRCYSVYCKKIHA- 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82;
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  Adeno-Associated Virus Vectors Encoding Methods of Using the Same
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19.0%; Pred. No. 1.1;
%ative 59; Mismatches 111; Indels 180;
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                       Factor
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RESULT 6
US-09-78-522-1
; Sequence 1, Application US/09978522
; Publication No. US20030033627A1
; GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/10/095,718
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 09/689,430
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/158,780
PRIOR FILING DATE: 1999-10-12
NUMBER OF SEQ ID NOS: 5
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Best Local S
Matches 133
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TYPE: PRT
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les 133; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----PVSVGCFVGFDASEPDSRHVVSIGKLKDIRFMSIFRFKVWWTTHWVGRNGGDL---- 113
                                                                                                                                                                                                                                                                                                                                                                                                                    GNGVIASME-----HCNDFMFLGTEAI----SLGRVGDDFW-------
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                                                                                                                                                                           RSEYYALPTROCLFEDPLHNGETMLKIWNLNKFTGVIGAF
                                                                                                                                                                                                                                                       GNFIHPDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLV---LPDGSIL 561
                                                                                                                                                                                                                                                                                                                                                                             GETVFMSMENPGLWVLGCHNSDFRNRGMTALLKVSSCNRNIDDYYEDTYEDIPTPLLNEN
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                                                                                                                                                                                                                                                                                                                                      -----CTDPSG-----DPNGTFWLQGC-----HMVHCANDSLWM 504
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19.0%; Pred. No. 8.
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PRIOR FILING DATE: 2000-10-16
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 862
TYPE: PRT
ORGANISM: Vitis LOX 1
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US-10-193-295-4
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                                                         Sequence 4, Application US/10193295
Patent NO. US20020173018A1
GENERAL INFORMATION:
APPLICANT: GONG, Fangcheng et al.
TITLE OF INVENTION: ACID MOLECULES ENCODI
TITLE OF INVENTION: ACID MOLECULES ENCODI
TITLE OF INVENTION: THEREOF
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APPLICANY: Irelan, Nancy
TITLE OF INVENTION: Lipoxygenase Genes From Vitis Vinifera
FILE REFERENCE: 29520/37890
CURRENT APPLICATION NUMBER: US/09/978,522
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 60/241,220
PRIOR FILING DATE: 2000-10-16
CURRENT APPLICATION NUMBER: US/10/193,295
CURRENT FILING DATE: 2002-07-12
                                     FILE REFERENCE: CL001195DIV
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                                                                               ENZYME PROTEINS, ENCODING HUMAN
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                                                                               ENZYME PROTEINS,
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RESULT 8
US-10-121-032-28
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PRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASTSEQ for Windows Versior
SEQ ID NO 4
LENGTH: 520
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                 Patent No. US20020155550A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 28, Application US/10121032
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                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:

ADDRESSEE: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
PRIOR APPLICATION DATA:
APPLICATION NUMBER
                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: GLYCOSIDASE ENZYMES NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bylina, Edward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GEDVGFKYDQDQ 760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VGIVALEIYFPSQYVDQAELEKYDGVDAGKYTIGLGQAKMGFCTDREDINSLCMTVVQNL 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -EDTYFDRDVEK 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLVQKSL -- ARMLLNDFLN -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNPKDIEWHSGENPISIEGVKTFALYLYQAKKLILSKPSQDLDIALDPFEFELITVSPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----CYLSALDRCYSVYCKKIHA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWCRETRRNQCFSQYSKRVTSK 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGNARPTGGVGAVALLIGPNAPLIFERGLRGTHMQHAYDFYK----PD----MLSEY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISLGRVGDDFWCTDPSGDPNGTFWLQGCHMVHCANDSLWMGNFIHPDWDMFQSTHPCAAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MERNNLSYDCIGRLEVGTETIIDKSKSVKTNLMQLFEESGNTDIEGIDTTN-ACYGGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----QW-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                    CLASSIFICATION: <Unknown>
                                                APPLICATION NUMBER: US/10/121,032 FILING DATE: 09-Apr-2002
                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                        COUNTRY: USA
ZIP: 92121
                                                                                                                                                                                                                              STATE: CA
                                                                                                                                                                                                                                          CITY: San Diego
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18.8%;
 NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --NAVNWIE-----
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 US/09/134,078
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 520
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Best Local S
Matches 138
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INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                          543
                                                                                                                                                                                                                                                                                                                490
                                                                                                                                                                                                                                                                                                                                                                                                                                                    399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 PFRTSIQPGDDDFVDVCVESGSSKVVDASFRSMLYLHAGDDPFALVK------- 187
                                                                                                                                                                             554 GSINY------DGKLIKS--FALDPEETINYAACHDNHTLWDKNYLAAKADKKKEWT 602
                                                                                                                                                                                                                                                                                                                                                                                                       453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            412 --LLEMLCED-----YGGRVDLAKAYYKAMTKSINKHFKGNGVIASME------ 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     355 PVLSPGLQMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGIDGVKIDVIH--- 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        311 GLSHLVELG------VTH------332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235 GVRHLVDGGCPPGLVLIDDGWQSIGHDSDPITKEGMNQTVAGEQMPCRLLKFQENYKFRD 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 GPKIEGYEDAIIYEIHIADITGLENS---GVKNK-----GLYLGLTEENTKGPGGVTT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224 KIRTTVDP-----YSKAV-----YANNQESAVVNLARTNPEGWENDR 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 FRVWSPVSKWVKVLLFKNGEDTE-PYQVVNMEYKGNGVWEAVVEGDLDGVFYLYQLENYG 223
                                                                                                                                                                                                                                                                                                                                                           451 YWVKEYHIDGFRFDQMGLIDKKTMLEVERALHKIDPTIILYGEPWGG-WGAPIRFGKSDV 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295 YVNPKATGPRAGQKGMKAFIDELKGEFKTVEHVYVWHALCGYWGGLRPQVPGLPEARVIQ 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97 FKVW-----WTTHWVGRNGGDLESETQIVILEKSDSG------RPYVFLLPIVE--G 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 138; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 09010/024002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858/677-1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     -----HCNDFMF--LG-TEAISLGRVGDDFWCTDPS----GDPNGTFW------L 489
                                                                                                                                                                                                                                                                                                                                                                                                                                               YGIGELSAFDQTVPYYFYRIDKTGAY------LNESGCGN-VIASERPMMRKFIVDTVT 450
SYNAPISING 651
                                          SGENPISIEG 647
                                                                                      EEELKNAQKLAGAI-LLTSQGVPFLHGGQDFCRTTNFND---
                                                                                                                                ----NLNKFTGVIGAFNCQG-----GG--WCRETRRNQCFSQYSKRVTSKTNPKDIEWH 637
                                                                                                                                                                                                                       GKHNFDLLKKLVLPDGSILRSEYYALPTRDCLFEDPLHNGETM------LKIW- 589
                                                                                                                                                                                                                                                                    AGTH-VAAFNDE-----FRDAIRGSVFNPSVKGFVMGG--YGKETKIKRGVV 553
                                                                                                                                                                                                                                                                                                              QGCHMVHCANDSLWMGNFIHPDWDMFQSTHPCAAFHAASRA-ISGGPIYVSDS-----V 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DPKNPHTRI-----GI-GVIMDMVFPHT 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----TG------DELDKDF---EKYYNW------GYDPYLFMVPEGRYST 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----EAMKIVRTHLGTERLLEEKTPPGIVDKFGWCTWDAFYL-----TVHPQGVIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 13-AUG-1998
APPLICATION NUMBER: 08/949,026
FILING DATE: 10-OCT-1997
APPLICATION NUMBER: 60/056,916
FILING DATE: 06-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Haile, Lisa A. REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 772 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.3%; Score 96; DB 9; Length 772; 20.6%; Pred. No. 4.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                      --N 641
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RESULT 10
US-09-773-753-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION UNMBER: U5/09/771,161A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-16-15
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 135619
PRIOR PILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ. ID NOS: 273
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US-09-771-161A-173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/09773753 Patent No. US20020099177A1 GENERAL INFORMATION:
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Best Local (
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SEQ ID NO 173
LENGTH: 344
TYPE: PRT
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                                       COUNTRY: USA
21P: 20005-5934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/773,753
FILING DATE: 02-Feb-2001
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 LYL-----HAGDDPFALVKEAMKIVRTHLGTFRLLEEKTPPGIVDKFGWCTWDAFYLTVH 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 ETQIVILEKSDSGRPYVFLLPIVEGPFRTSIQPGDDDFVDVCV--ESGSSKVVDASFRSM 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        289 GFLPNGSLEDRLHCQTQACPP 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 ESSVSLLQ---GARPSPFCWPLCE-----ISRGTHNFSEELKIGEGGFGCVYRAVMRNT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 27.0% nes 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: HUMAN IRAK-2
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: NI, JIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VYAVKRLKENADLEWTAVKQSFLTEVEQLSRFR-----HPNIVDFAGYCAQNGFYCLVY 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---PQGVIEGVRHLVDGGCPP 246
                                                                                                                                                                                                                                                                                                                           CITY: WASHINGTON STATE: D.C.
                        APPLICATION NUMBER: 08/980,060
FILING DATE: <Unknown>
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DIXIT, VISHVA M.
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                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 262
LENGTH: 712
TYPE: PRT
                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/771,161A CURRENT FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: LEVINE, et al. TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES FILE REFERENCE: 802620-2005.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 135619
                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
    289
                                                                                                                    174 LYL-----HAGDDPFALVKEAMKIVRTHLGTFRLLEEKTPPGIVDKFGWCTWDAFYLTVH 228
                                                                                                                                                                 184
                                                                                                                                                                                                     116 ETQIVILEKSDSGRPYVFLLPIVEGPFRTSIQPGDDDFVDVCV--ESGSSKVVDASFRSM 173
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                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
TOPOLOGY: No. US20020099177A1 Relevant
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
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                                      ---PQGVIEGVRHLVDGGCPP 246
GFLPNGSLEDRLHCQTQACPP 309
                                                                              VYAVKRLKENADLEWTAVKQSFLTEVEQLSRFR-----HPNIVDFAGYCAQNGFYCLVY 288
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                                                                                                                                                             ESSVSLLQ---GARPSPFCWPLCE----ISRGTHNFSEELKIGEGGFGCVYRAVMRNT 234
                                                                                                                                                                                                                                             38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 712 amino acids
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27.0%;
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                                                                                                                                                                                                                                         16; Mismatches
                                                                                                                                                                                                                                                                Score 95.5; DB 10; Pred. No. 4.7;
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US-09-771-161A-264
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US-09-771-161A-263
                                                                                                                                                                                   SEQ ID NO 264
LENGTH: 712
TYPE: PRT
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Best Local Similarity 27.0%;
Matches 38; Conservative 1
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APPLICANT: LEVINE, et al.
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                                                               Matches
                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: U
CURRENT FILING DATE: 2001-01
                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 136776
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TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
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PRIOR EILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
                                                                                                                                                              ORGANISM: Homo sapiens
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                  116 ETQIVILEKSDSGRPYVFLLPIVEGPFRTSIQPGDDDFVDVCV--ESGSSKVVDASFRSM 173
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                                                                                Local Similarity
  Application US/09771161A
                                                             Conservative
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                                                                              2.3%; Score 95.5; DI 27.0%; Pred. No. 4.7;
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Pred. No. 4.7;
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RESULT 14
US-10-101-464A-954
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PRIOR FILING DATE: 2000-11-01
PRIOR PPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 2000-01-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Strabala, Timothy APPLICANT: Nieuwenhuizen, N
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                                                                                                                               LQILIALSNYLLGPIPESL---GKCRSLERI--
                                                                                                                                                                                                              ELKGEFKTVEHVYVWHALCGYWGGLRPQ-VPGLPEARVIQ-----PVLSPGL----QM 363
                                                                                                                                                                                                                                                                                                                                                                                 RLDAASCGLSGE-IPPEIAKLQNLDTLFLQVNGFAGSLPAEIGYLNSLKSLDLSNNMFAG
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    ----SVGKHNFDLLKKLVLPDGSILRSEYYALPTRDCLFEDPLHNGETMLKI-WNLN
                                         PRGLFGLPELNQVE-FQDNLLVGEFPVSD-------DSIALKLGQITLSNNK 474
                                                                                   PNGTFWLQGCHMVHCANDSLWMGNFIHPDWDMFQSTHPCAAFHAASRAISGGPIYVSD--
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Best Local Similarity
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SEQ ID NO 2
LENGTH: 26926
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09759508B Publication No. US20020182599A1 GENERAL INFORMATION:
APPLICANT: Fishman, Mark C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Methods for Diagnosing and Treating Heart Disease FILE REFERENCE: 00786/381002 CURRENT APPLICATION NUMBER: US/09/759,508B CURRENT FILING DATE: 2001-01-12 PRIOR APPLICATION NUMBER: US 60/175,787 PRIOR FILING DATE: 2000-01-12 NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                             13515 PSVSW------KKGEDPLATDTRVSVESSAVNTTLIVYDCQKSDAGK-YTTTLKNVAGT 13566
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                                         13710 ITGYHLEFKERNSLLWKRANKTPIRMRDF---KVTGLTEG------LEYEFRVM-- 13754
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VYVWHALCGYWGGLRPQVPGLPEARVIQPVLSPGLQMTMEDLAVDKIVLHKVGLVPPEKA 386
                                                                                 MPCRLLKFQEN-----YKFRDYVNPKATGPRAGQKGMKAFIDELKGEFKTVEH 326
                                                                                                                                                                  PQGVIEGV-----RH---LVDGGCPPGLVLIDDGWQSIGHDSDPITKEGMNQTVAGEQ 278
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Indels 194;

Gaps

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Db 13755 -----AINLAGVGKPSLPSEPVV-ALDPIDPPGKP------EVINITRNSVTLI----WT 13798

Oy 387 EEMYEGLH 394

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Db 13799 EPKYDGGH 13806

Search completed: April 4, 2003, 11:18:14

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SUMMARIES

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ALIGNMENTS

TITLE	REFERENCE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	E15707	RESULT 1
RAFFINOSE SYNTHASE GENE, PRODUCTION OF RAFFINOSE AND TRANSFORMED Patent: JP 1998084973-A 1 07-APR-1998; AJINOMOTO CO INC	unclassified. 1 (bases 1 to 2517) Occumic C Novaki 1 and Kida T	unidentified	unidentified.	JP 1998084973-A/1.	E15707.1 GI:5710390	E15707	Cucumis sativus mRNA for raffinose synthase, complete cds.	E15707 2517 bp DNA linear PAT 28-JUL-1999		

Pred. No.

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PN JP 1998084973-A/1
PD 07-APR-1998
PF 28-APR-1997 JP 1997111124
PR 26-APR-1996 JP 96P 107682, 26
PR 26-APR-1997 JP 107682, 26
PR 26-APR-1997 JP
GACGCGTTTTACCTAACGGTTCATCCACAGGGCGTAATAGAAGGCGTGAGGCATCTCGTC
                                   CGCTTGTTGGAGGAGAAGACTCCACCAGGTATCGTGGACAAATTCGGTTGGTGCACGTGG
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        transformed plant
patent; JP 199123080-A 1
AJINOMOTO CO INC
OS Cucumis sativus (Cuc
PN JP 1999123080-A/1
PD 11-MAY-199
PF 24-OCT-1997 JP 19972
PR CHIEKO OZUMI, JINJI N
PC C12N15/09, AOH5/00, C
Strandedness: Double;
CC Topology: Linear,
FH Key
CDS 56.
                                                                                                                                   Cucumis sativus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eu

Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Cuc

1 (bases 1 to 2569)

Chieko,O., Jinji,N. and Takao,K.

Raffinose synthase gene, process for producing raffir
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JP 1999123080-A/1.
                                                                                   Cucumis sativus (Cucumber) JP 1999123080-A/1 11-MAY-1999
                                    CHIEKO OZUMI,JINJI NOZAKI,TAKAO KIDA
C12N15/09,A01H5/00,C12N9/00//(C12N9/00,C12R1:19)
Andedness: Double;
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56. .2407.
Location/Qualifiers
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.

1 (bases I to 2569)

Ohsumi, C., Nozaki, J. and Kida, T.
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Submitted (22-JUN-1998) Central Research Laboratories, Aajinomoto
Co. Inc., 1-1, Suzuki-cho, Kawasaki-ku, Kawasaki 210-8681, Japan
Location/Qualifiers
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1010	Оу 961	Oy 901	Oy 841	Оу 781 Db 836	Qy 721 Db 776	Qy 661 Db 716	Qy 601	Qy 541 Db 596			Oy 361	Oy 301	Oy 241	Oy 181	Oy 121 Db 176	Qy 61 Db 116	Qy 1	Query Mai Best Loca Matches
	TTTAAGACTGTGGAGCATGTTTATGTTTGGCATGCTTTGTGTGGGATATTGGGGTGGCCTT 1	01 ACCGGCCCCGAGCCGGCCAGAAGGGGATGAAGGCGTTTATAGATGAACTCAAAGGAGAG 960 		81 GATTCGGATCCCATCACCAAAGAAGGAATGAACCAAACCGTCGCCGGCGAGCAAATGCCC 840	21 GACGGCGGTTGTCCTCCCGGTTTAGTCCTAATCGACGATGGTTGGCAATCCATCGGACAC 780 	GACGCGTTTTACCTAACGGTTCATCCACAGGGCGTAATAGAAGGCGTGAGGCATCTCGTC	01 CGCTTGTTGGAGGAGAAGACTCCACCAGGTATCGTGGACAAAATTCGGTTGGTGCACGTGG 660		GGTTCGTCGAAAGTTGTTGATGCATCGTTCCGAAGTATGTTGTATCTTCATGCTGGTGAT	CCGTTCCGAACCTCGATTCAGCCTGGGGATGATGATGTTTGTCGATGTTTGTGTCGAGAGT	61 ATCCTTGAGAAGTCAGATTCTGGTCGACCGTATGTTTTCCTTCC	4-4	ര – ര	81 CCGGTTTCGGTTGGTTGGTTTGGATTCGACGCGTCGGAACCTGATAGCCGACATGTT 240			1 ATGGCTCCTAGTTTTAAAAATGGTGGCTCCAACGTAGTTTCATTTGATGGCTTAAATGAC 	Match 100.0%; Score 2352; DB 8; Length 2569; Local Similarity 100.0%; Pred. No. 0; es 2352; Conservative 0; Mismatches 0; Indels 0; Gaps
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Qy	Db Qy	Db Qy		da V	Db Qy		Db	Db	Ор	Qу	Db		рь	рь	D Qy		Qу	Qу
2101 GGGCTGGTGAACATGCTTAACACTAGTGGAGCCATCCAATCTGTGGACTATGACGATGAC 2160	2041 CTCATCACTGTTTCACCAGTGACCAAACTCATCCAAACTTCTCTACACTTTGCCCCAATT	1981 CTTATCCTCTCCAAGCCCTCTCAAGATCTTGACATAGCTCTTGACCCATTCGAGTTCGAGT 	> - >	16 T	4 4 - 1	≱-≥	1681 CTTCGAAGTACTATGCACTCCCGACTCGCGATTGTTTGTAGAAGACCCTTTGCAT [보드년	1561 TGTGCCGCCTTCCATGCTGCCTCTCGAGCCATCTCTGGTGGCCCGATCTATGTTAGTGAT	1501 AGCTTGTGGATGGGGAACTTCATCCACCCTGACTGGGATATGTTCCAATCCACCCAC	1441 GGTGATCCAAACGGTACGTTTTGGCTCCAAGGATGTCACATGGTTCATTGTGCCAACGAC	ი – ი	ე-ე	ი – ი	201 G 1 256 G	141 G 196 G	1081 CTGCAGATGACGATGGAGGATTTGGCGGTGGATAAGATTGTTCTTCATAAGGTCGGGCTG	8=8

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S Eljiro, W. and Kenji, O.

Raffinose synthase gene

L Patent: JP 2000014389-A 1 18-JAN-2000;

SUMITOMO CHEM CO LTD

OS Brassica juncea

PN JP 2000014389-A/1

PD 18-JAN-2000

PF 10-DEC-1998 JP 1998351246

PR EIJIRO WATANABE, KENJI OEDA

PC C12N15/09, A01H5/00, C12N1/21, C12N5/10, C12N9/88, C1201/68// PC

(C12N9/88, C12R1:91), C12N15/00, C12R1:91), CC

(C12N9/88, C12R1:91), C12N15/00, C12N15/00, C12R1:91) CC

FH Key

FT CDS

Location/Qualifiers

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TTGGGAAGCTGAAGGATATTCGGTTTATGAGTATTTTCAGGTTTAAGGTTTGGTGGACTA
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Raffinose synthase gene E36417.1 GI:13019215
JP 2000014389-A/1.

Brassica juncea.
Brassica juncea
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E. Raffinose synthase gene
NAL Patent: JP 200016652-A 1 20-JUN-2000;
SUMITOMO CHEM CO LTD

OS Beta vulgaris L.

PN JP 200016562-A/1

PD 20-JUN-2000

PF 04-DEC-1998 JP 1998345590

PR
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PC (C12N15/09, C12N1/21, C12N15/10, C12N15/09, PC (C12N9/88, C12R1:91),

PC (C12N9/88, C12R1:91). C12N15/09
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1127 1362	1068 GCTTTCACCAGGGCTGCAGATGACGATGGAGGATTTGGCGGTGGATAAGATTGTTCTTCA	
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830 1062	774 CGGACACGATTCGGATCCCATCACCAAAGAAGGAATGAACCAAACCGTCGCCGGCGA	
773 1002	714 TCTCGTCGACGGCGGTTGTCCTCCCGGTTTAGTCCTAATCGACGATGGTTGGCAATCCAT	
713 942	654 CACGTGGGACGCGTTTTACCTAACGGTTCATCCACAGGGCGTAATAGAAGGCGTGAGGCA	
653 882	594 AACTTTTCGCTTGTTGGAGGAGAAGACTCCACCAGGTATCGTGGACAAATTCGGTTGGTG	
593 822	534 TGGTGATGATCCGTTTGCACTTGTTAAAGAGGCGATGAAGATCGTGAGGACCCATCTTGG	
533 762	474 CGAGAGTGGTTCGTCGAAAGTTGTTGATGCATCGTTCCGAAGTATGTTGTATCTTCATGC	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mutant protein, its DNA and use thereof Patent: JP 2001078783-A 1 27-MAR-2001; SUMITOMO CHEMICAL CO LITD OS Glycine max (soybean) PN JP 2001078783-A/1 PD 27-MAR-2001 JP 2000200571 PF 03-JUL-2000 JP 2000200571 PF C12NI5/09,A01H5/00,C12NS/10,C12N9/10,C12N5/00 CC C12NI5/09,A01H5/00,C12NI5/00 CC FH Key Location/Qualifiers FT CDS Location/Qualifiers
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                                     GACCCATCTTGGAACTTTTCGCTTGTTGGAGGAGAAGACTCCACCAGGTATCGTGGACAA
                                                                       ATACGTCCACGTTGGCCATGACCCGTATCAGTTGCTTAGAGAAGCAACTAAAGTCGTTAG
                                                                                       GTATCTTCATGCTGGTGATGATCCGTTTGCACTTGTTAAAGAGGCGATGAAGATCGTGAG
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
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Raffinose synthase gene a
Patent: JP 199215984-A
SUMITOMO CHEM CO LTD
OS Glycine max(soybean)
PN JP 199215984-A/2
PD 10-AUG-1999
PF 12-DEC-1997 JP 19973
PR EIJIRO WTANABE, KENJI
PC C12N15/09, CO7K14/415
C12O1/527,
PC C12N15/00, C12R1:91)
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Raffinose synthase gene a
E24424
E24424.1 GI:13018164
JP 1999215984-A/2.
Glycine max.
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C12N15/09,C07K14/415,C07K16/16,C12N1/21,C12N5/10,C12N9/88, PC
C12N15/00,
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JP 1999215984-A/2
                                      C1201/68,G01N33/573//(C12N15/09,C12R1:91),(C12N1/21,C12R1:19),(C12N5/10,C12R1:91),(C12N9/88,C12R1:19),
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                                                                     CGTCGCCGGCGAGCAAATGCCCTGCCGTCTTTTGAAATTCCAAGAGAGATTACAAATTCCG
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                          TGACTACGTCAATCCCAAGGCCACCGGCCCCCGAGCCGGCCAGAAGGGGGATGAAGGCGTT
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CC Topology: Linear
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Submitted (09-JAN-2002) Peterbauer T., Institute of Ecology,
University of Vienna, Althanstrasse 14, Vienna, A-1090, AUSTRIA
On Jan 16, 2002 this sequence version replaced gi:18071124.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                          Peterbauer T.
Direct Submission
Submitted (02-JAN-2002) Peterbauer T.,
University of Vienna, Althanstrasse 14,
revised by [3]
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/protein_id="CAD20127.2"
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148. .2544
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                                         AGGCTTATAAAATATGAAGAGAATTATAAATTTAGAGAATACGAAAAT------
                                                                                                                                                   TGTCCTCCGGGTTTCGTCATAATCGACGACGGTTGGCAATCCATTTCTCATGATGATGAT
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/translation="mappsitkinatqodvistudignspllsisldqsrnflunghpf
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"WKIGVRGCGELSVFASEKPVCCKIDGVSVEFDYEDKMYRVQILMPGSSTLSLVEFLF
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Pred. No. 2.9e
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1.9e-274;
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                                                                                                                                                                      GCCGCCTTCCATGCTGCCTCTCGGAGCCATCTCTGGTGGCCCGATCTATGTTAGTGATTCT 1623
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                                                                                                                TCACACGCGGTGACATGTTATGCAAGTCCTGAAGATATTGAATGGTGCAATGGAAAAACC
                                                                                                                                                                                                                                                                                                                                               GTTGGTAATCACAATTTCAAGTTGCTCAAATCTTTTGTTTTTGCCCGACGGTTCTATCTTG
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AGTCTCATGAAGTGTTCCGATAGATTGGAAGTTTCGCTCGAGCCATTTAGTTTTGAGCTA
                                                        CCAATGGACATCAAAGGTGTGGATGTTTTCGCTGTGTATTTTTTCAAGGAGAAGAAACTG
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AUTHORS
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ORGANISM
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DEFINITION
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L Patent: JP 199215984-A 1 10-AUG-1999;
SUMITOMO CHEM CO LTD
OS Vicia faba(broad bean)
PN JP 199215984-A/1
PD 10-AUG-1999
PF 12-DEC-1997 JP 1997342899
PF 22-DEC-1997 JP 1997342899
PC C12N15/09,C07K14/415,C07K16/16,C12N1/21,C12N5/10,C12N5/27,
PC C12N15/09,C07K14/415,C07K16/16,C12N1/21,C12N5/27,
PC C12N5/10,C12R1:91),(C12N15/09,C12R1:91),(C12N1/21,C12N1/21),(C12N5/10,C12R1:91),(C12N1/21),(C12N5/10,C12R1:91),(C12N1/21),(C12N5/10,C12R1:91),(C12N1/21),(C12N5/10,C12R1:91),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1/21),(C12N1
                                                               GGTTGCTTTGTTGGATTCGACGCGTCGGAACCTGATAGCCGACATGTTGTTTCGATTGGG 252
AAGCTGAAGGATATTCGGTTTTATGAGTATTTTCAGGTTTTAAGGTTTTAGGTGGACTACACAC
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E24423.1 GI:13018163
JP 1999215984-A/1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eijiro, W. and Kenji, O.
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C12N15/09,C07K14/415,C07K16/16,C12N1/21,C12N5/10,C12N9/88,
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/db_xref="taxon:3906"
552 c 621 g
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Location/Qualifiers
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Pred. No. 2.9e-274;
0; Mismatches 694;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; eudicotyledons; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Salk, Stanford, PGEC (SSP) Consortium members carried out sequencing and annotation of the RAFL CONAs: Nguyen, M., Southwick, A., Karlin-Neumann, G., Lam, B., Miranda, M., Palm, C.J. Bowser, L., Jones, T., Banh, J., Chen, H., Cheuk, R., Chung, M.K., Kim, C., Lin, J., Liu, S.X., Pham, P.K., Sakano, H., Shinn, P., Kim, C., Lin, J., Liu, S.X., Pham, P.K., Sakano, H., Shinn, P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (27-FEB-2002) DNA Sequencing and Technology Center,
Submitted University, 855 California Avenue, Palo Alto, CA 94304,
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Southwick, A., Karlin-Neumann, G., Nguyen, M., Lam, B.,
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~	7	TTCTGGTCGACCGTATGTTTTCCTTCTTCCGATCGTTGAGGGACCGTTCCGAACCTCG 4	
٥	403	GGTCGGGTCGTTATGTTCTCTTGCTACCTCTTCTTGAAGGCTCCTTCCGTTC!	2
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~	556	TTAAAGAGGCGATGAAGATCGTGAGGACCCCATCTTGGAACTTTTCGCTTGGTTGG	G
O	583	TTCAAGCTTCTTGAAG	2
`	616	CACCAGGTATCGTGGACAAATTCGG	υī
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`	796	AAGGAATGAACCAAACCGTCGCCGGCGAGCAAATGCCCTGCCGTCTTTTC	Ūι
Ü	823	GATGTCGAAGGGATGAATATTACCGTCGCCGGTGAACAAATGCCTTGCAGGCTTCTGAAG 88	2
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Submitted (14-NOV-2001) DNA Sequencing and Technology Center, Submitted (14-NOV-2001) BNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Nguyen, M., Southwick, A., Karlin-Neumann, G., Lam, B., Miranda, M., Palm, C.J., Bowser, L., Jones T., Banh, J., Chen, H., Cheuk, R., Chung, M.K., Kim, C., Lin, J., Liu, S.X., Pham, P.K., Sakano, H., Shinn, P., Yamada, K., Ecker, J., Theologis, A. and Davis, R.W.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 2718)
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GIVDKFGWCTWDAFYLTVNPDGVHKGVKCLVDGGCPPGLVLIDDGWQSIGHDSDGIDV
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WHALCGYWGGLRPEAPALPPSTIIRPELSFGLKITMEDLAVDKIIETGIGFASPDLAK
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GVIASMEHCNDFMFLGTEAISLGRVGDDFWCTDPSGDDNGTFWLQGCHXVHCAYNSLM
MGNET DPDMDMFQSTHCGTEAISLGRVGDDFWCTDPSGDDNGTFWLQGCHXVLCAYNSGIL
RCEYYALDTRDRLFEDPLHDGKTMLKTTGVIGAFNCOGGGGCRETRRQCFS
ECVNTLTATTSPKDVEWNSGSSPISIANVEEFALFLSQSKKLLLSGLNDDLELTLEPF
KFELITVSPVTIEGNSVFAPIGLVMNLNTTSGAIRSLVNDESVEVGVFGAGEFRVY
ASVENDVEGTIFFCTUDEFCVFFAPIGLVMNLNTTSGAIRSLVNDESVEVGVFGAGEFRVY
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132. .:
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                           ASKKPVSCLIDGEVVEFGYEDSMVMVQVPWSGPDGLSSIQYLF"
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/db_xref="taxon:3702"
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PC C1201/527,

PC C1201/58,G01N33/573//(C12N15/09,C12R1:91),(C12N1/21,C12R1:19),

PC C1201/58,G01N33/573//(C12N15/09,C12R1:91),(C12N1/21,C12R1:19),

PC C1201/50,(C12R1:91),(C12N9/88,C12R1:91),(C12N9/88,C12R1:19),

PC C12N15/00,(C12N15/00,C12R1:91),(C12N5/00,C12R1:91)

PC C12N5/00,(C12N15/00,C12R1:91),(C12N5/00,C12R1:91)

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PC C12N15/09,A01H5/00,C12N1/21,C12N9/88,C1201/68// PC

(C12N1/21,C12R1:91),C12N15/00,C12R1:91),(C12N9/88,C12R1:91), PC

(C12N9/88,C12R1:91),C12N15/00,C12N15/00,C12N15/00,C12R1:91) CC

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                                                            TTGGAAGAAAAACGCCGCCGGGAATCGTCGATAAGTTCGGGTGGTGCACGTGGGATGCG
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E36418.1 GI:13019216
JP 2000014389-A/2.
Brassica napus.
Brassica napus
Brassica piridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; Brassicaceae; Brassica.
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AAACGAGTGACATCCAAAACTAACCCAAAAGACATAGAATGGCACAGTGGAGAAAACCCT
                                                          TGCCAAGGAGGATGGTGTCGTGAGACACGCCGCAACCAATGCTTTTCACAATACTCA
                                                                                        AAAACCATGCTCAAGATTTGGAACTTGAACAAGTACACTGGAATCATCGGAGCATTCAAC
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Chain Elongation of Raffinose in Pea Seeds: ISOLATION,
CHARCTERIZATION, AND MOLECULAR CLONING OF A MULTIFUNCTIONAL
CATALYZING THE SYNTHESIS OF STACHYOSE AND VERBASCOSE
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/codon_start=1
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SFSSICKPSESNAPPSLLQKVLAYSHKGGFFESHETPSDFLMNSIGSFNGKDFLSIF
RFKTWMSTQWIGKSGSDLQMETQWILIEVPETKSYVVIPIIIIEKFRSALFPGFNDHV
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                    TGCCATGGCCAATTGATTCTT
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2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT: *
3: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT: *
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ALIGNMENTS

AAH24065 ABK69837

AAA53450 ABN79093

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AAX61259 ABL73625 AAH87794

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AAV40803 AAZ10004 AAC42001

Corn raffinose syn Rice raffinose syn Wheat raffinose sy Wheat raffinose syn Corn raffinose syn Corn raffinose syn Corn raffinose syn Nucleic acid encod Arabidopsis thalia Arabidopsis

AAD00333 AAD00331 AAD00338 AAD00337

RESULT 1
AAV22250
ID AAV2

AAV22250 standard; cDNA to mRNA; 2517 BP

Cucumber; raffinose synthase; sucrose; galactinol; ds

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NA1995.DAT:*	AC A	AAV22250:	
NA1996.DAT:*	××		
NA1997.DAT:*	DT	06-JUL-1998 ((first entry)
NA1998.DAT:*	××		•
NA1999.DAT:*	DE	Cucumber raffi	Cucumber raffinose synthase cDNA.
NA2000.DAT:*	XX		
NA2001A.DAT:*	K₩	Cucumber; rafi	Cucumber; raffinose synthase; sucrose; galactinol
NA2001B.DAT:*	XX		,
NA2002.DAT:*	SO	Cucumis sativus	IS.
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ce to have a	HA	Key	Location/Qualifiers
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bution.	FT		/*tag= a
	FT		/product= raffinose_synthase
	××		
	Nd	JP10084973-A.	
	××		
Description	PD	07-APR-1998.	
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Cucumber raffinose	PF	28-APR-1997;	97JP-0111124.
Cucumber raffinose	××		
Mustard raffinose	PR	26-JUL-1996;	96JP-0198079.
Soybean raffinose	PR	26-APR-1996;	96JP-0107682.
Soybean raffinose	XX		
Sugarbeet raffinos	PA	(AJIN) AJINOMOTO KK.	IOTO KK.
Soybean polynucleo	xx		
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Broad bean raffino	DR	P-PSDB; AAW53570.	70.
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AAV22250 AAX61238 AAZ202090 AAV20801 AAC89523 AAC20208 AAH27438 AAH27438 AAZ10002 AAV40800

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Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2517 BP; 613 A; 524 C; 642 G; 738 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
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                               GGTTCGTCGAAAGTTGTTGATGCATCGTTCCGAAGTATGTTGTATCTTCATGCTGGTGAT
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1860	TTCAACTGCCAAGGAGGAGGATGGTGTCGTGAGACAGCCGCACCAATGCTTTTCACAA .	1801	Qy
1915		1856	Db
1800	AATGGAGAAACTATGCTTAAGATTTGGAATCTCAACAAGTTCACTGGAGTGATTGGTGCA	1741	Qy
1855		1796	Db
1740	CTTCGAAGTGAGTACTATGCACTCCCGACTCGCGATTGTTTGT	1681	Qy
1795		1736	Db
1680 1735	TCTGTGGGAAAGCATAACTTTGATCTTCTGAAAAAACTAGTGCTTCCTGATGGATCGATC	9 9	Дb
1620 1675	TGTGCCGCCTTCCATGCTGCCTCTCGAGCCATCTCTGGTGGCCCGATCTATGTTAGTGAT	் ப	Qy Db
1560	AGCTTGTGGATGGGGAACTTCATCCACCCTGACTGGGATATGTTCCAATCCACCCAC	1501	Qy
1615		1556	Db
1500	GGTGATCCAAACGGTACGTTTTGGCCTCCAAGGATGTCACATGGTTCATTGTGCCAACGAC	1441	Qy
1555		1496	Db
1440	GGCACGGAAGCTATCTCTCTGGTCGTGGTGTGATGACTTTTGGTGCACGGACCCCTCT	1381	Qy
1495		1436	Db
1380	CATTITAAAGGAAAIGGAGTCAFTGCAAGTATGGAACATTGTAACGACTTCATGTTCCTT	1321	Qy
1435		1376	Db
1320	GGAGGGAGAGTGGATTTGGCAAAAGCATATTACAAAGCAATGACCAAATCAATAAATA	1261	Qy
1375		1316	Db
1260 1315	GGGATCGACGGTGTTAAGATTGACGTTATCCACCTATTGGAGATGTTGTGTAGAGACTAT		Qy Db
1200	GTCCCGCCGGAGAAGGCTGAGGAGGATGTACGAAGGACTTCATGCTCATTTTGGAAAAAGTT	μ	Qy
1255			Db
1140	CTGCAGATGACGATGGAGGATTTGGCCGGTGGATAAGATTGTTCTTCATAAGGTCGGGCTG	1081	Qy
1195		1136	Db
1080 1135	CGCCCGCAGGTGCCTGGCTTGCCTGAGGCACGTGTGATTCAGCCAGTGCTTTCACCAGGG		Qy Db
1020	TTTAAGACTGTGGAGCATGTTTATGTTTGGCATGCTTTGTGTGGATATTGGGGTGGCCTT	961	Qy
1075		1016	Db
960	ACCGGCCCCGAGCCGGCCAGAAGGGGATGAAGGCGTTTATAGATGAACTCAAAGGAGAG	901	Qy
1015		956	Db
900	TGCCGTCTTTGAAATTCCAAGAGAATTACAAATTCCGTGACTACGTCAATCCCAAGGCC	841	Qy
955		896	Db
895	GATTCGGATCCCATCACCAAAGAAGGAATGAACCAAACCGTCGCCGGCGAGCAAATGCCC	836	DЬ

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e present invention describes a raffinose synthase, having an activity forming raffinose from sucrose and galactinol. The raffinose synthase ne can be used for expression in a plant for the production of
                                                                                               raffinose synthase cose and galactinol
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DB; AAY17417.
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30-APR-1998;
04-DEC-1998;
10-DEC-1998;
This is the nucleotide sequence of a mustard cDNA clone coding for raffinose synthase (see AAY32074), a protein which can bind a D-galactosyl group through an alpha(1-6) bond to the hydroxy group attached to the carbon atom at the 6-position of the D-glucose residue in a sucrose molecule to form raffinose. The cDNA was
                                                         New sense raffinose
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                                                                                                                 SUMITOMO CHEM
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isolated from mustard (Brassica juncea) leaf cDNA by PCR. Probes or primers generated from plant raffinose synthase genes (see AAZ20207-10) may be used to obtain other raffinose synthase genes by labeled detection or amplification (claimed). These genes may labeled to control the levels of raffinose produced in plants. Antisense genes can be used to knock out existing gene activity, and sense genes to increase the level of gene activity. The resulting transgenic plants may be used as a food source to alter the growing conditions for gut enterobacteria, providing general health advantages. The sense and antisense genes may also be used in gene and phenotypic analysis of plants and for the selection of reference with the desired characteristics with respect to raffinose content.

Sequence 2690 BP; 648 A; 608 ű 668 G; 765 T; 1 other;

Query Match Best Local Similarity Matches 1530; Conserv

Conservative

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Score 1041.4; pred. No. 0; o; Mismatches

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                                                    New nucleic acid molecule encoding plant raffinose synthetase capable of producing raffinose, used as food additives with beneficial effects on gastrointestinal flora
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 TGACTACGTCAATCCCAAGGCCACCGGCCCCCGAGCCGGCCAGAAGGGGGATGAAGGCCGTT
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Query Match
Best Local Similarity
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                                                                                                        GTGGCAAGCCATTTGTCACGACGAGGAGCACCATAACGGACCAAGAGGGTATGAAGCGAAC
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CTCCGCAGGGGAGCAAATGCCATGCAGGTTGGTGAAGTTGGAGGAAAATTACAAGTTCAG
                                                                                                                                                               TTGGCAATCCATCGGACACGATTCGGATCCCATCAC - - - CAAAGAAGGAATGAACCAAAC
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Pred. No. 8.4e-304;
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                 TTACCTCTATCAAGCCAAAAAACTTATCCTCTCCAAGCCCTCTCAAGATCTTGACATAGC
                                                                                                                   GAGAAACAAGAGTGCCTCTGAATTTTCACAAACTGTGACATGCTTAGCGAGTCCTCAAGA
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                                                                                                                                                                                                         30-APR-1999;
01-SEP-1999;
                                                                The present invention provides novel plant promoters which can be used the production of transgenic plants which express genes with desired
                                                                                                             New soybean plant promoters useful for with desired properties {\ \ }
                                                                                                                                         WPI; 2001-104537/12.
P-PSDB; AAB49400.
                                                                                                                                                                                                                                                       02-NOV-2000
                                                                                                                                                                                                                                                                        EP1048733-A2
                                                                                                                                                                                                                                                                                            Glycine
                                                                                                                                                                                                                                                                                                            Plant promoter;
                                                                                                                                                                                                                                                                                                                               Soybean raffinose synthase coding
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                                                                                                                                                                                                                                                                                                                                                                                      AAC89523 standard; DNA;
                                      Sequence
                                                                                            Example 2; Page 24-28; 36pp; English
                                                                                                                                                                     Ishige F,
                                                                                                                                                                                       (SUMO ) SUMITOMO CHEM CO LTD
                                                                                                                                                                                                                                     27-APR-2000;
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nilarity 66.0%;
Conservative
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99JP-0247211.
                                                                                                                                                                                                                                                                                                            transgenic
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Score 976.4; DB 22;
Pred. No. 1.3e-303;
0; Mismatches 741;
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                                     673 G;
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                                                                                                                                                                                                                                                                                                            desired property;
                                      653 T; 0 other;
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1178	1119 TGTTCTTCATAAGGTCGGGCTGGTCCCGCCGGAGAAGGCTGAGGAGGATGTACGAAGGACT	Qy
1118 1182	1059 TCAGCCAGTGCTTTCACCAGGGCTGCAGATGACGATGGAGGATTTGGCGGTGGATAAGAT	Qу ВЬ
1058 1122	999 GTGTGGATATTGGGGTGGCCTTCGCCCGCAGGTGCCTTGCCTTGACCTTGAGCACGTGTGAT	Qу
998 1062	939 TATAGATGAACTCAAAGGAGAGTTTAAGACTGTGGGAGCATGTTTATGTTTGGCATGCTTT	ОУ
938 1002	879 TGACTACGTCAATCCCAAGGCCACCGGCCCCGAGCCGGCAGAAGGGGATGAAGGCGTT	ОУ
878 957	9 GTCGCCGGCGAGCAAATGCCCTGCCGTCTTTGAAATTCCAAGAGAATTACAAATTCCG III IIIIIIIIII IIIIIIIIIIIIIII	Qу
818 897	762 TTGGCAATCCATCGGACACGATTCGGATCCCATCACCAAAGAAGGAATGAACCAAAC	Db
761 837	ACGATGG ACGACGG	da Vo
701 777	.42 ATTCGGTTGGTGC2 18 GTTTGGTTGGTGT1	Оу
641 717	POTTGGAACTTTTCGCTTGTTGGAGAGAAGACTCCACCAC 	Оy
581 657	522 GTATCTTCATGCTGGTGATGATCCGTTTGCACTTGTTAAAGAGGCGATGAAGATCGTGAG	Оy
521 597	462 CGATGTTTGTGTCGAGAGTGGTTCGTCGAAAGTTGTTGATGCATCGTTCCGAAGTATGTT	Оy
461 537	402 TCTTCCGATCGTTGAGGGACCGTTCGAACCTCGATTCAGCCTGGGGATGATGACTTTGT	Оy
401 477	345 GGAGACTCAGATTGTGATCCTTGAGAAGTCAGATTCTGGTCGACCGTATGTTTTCCT	Оy
344 417	285 CAGGTTTAAGGTTTGGTGGACTACACACTGGGTTGGAATGGTGGGGGATCTTGAATC	. Db
284 357	225 TGATAGCCGACATGTTGTTTCGATTGGGAAGCTGAAGGATATTCGGTTTATGAGTATTTT	Qy Db
224 297	165 TTCGATAGACAAGTCCCCGGTTTCGGTTGGTTTGTTTGGATTCGACGCGTCGGAACC	Оу
164 237	117 TCTGTCCGATGTTCCTGAGAACATTGTTGCTTCTCTCTCT	Qу
177		Ъ

2258	GATGCGAGTATTTGCATCGAAAAAACCAAGGGCTTGTCGTATTGATGGGGAGGATGTTGG	2199	dd
2322		2263	Vy
2198	ATCTGTGGACTATGACGATGACCTAAGCTCAGTCGAGATTGGTGTCAAAGGGTGTGGTGA	2139	Qy
2262		2203	Db
2138 2202	TICTCTACACTTTGCCCCAATTGGGCTGGTGAACATGCTTAACACTAGTGGAGCCATCCA	2079 21 4 3	ДУ
2078 21 4 2	TCTTGACCCATTCGAATTCGAGCTCATCACTGTTTCACCAGTGACCAAACTCATCCAAAC	2019 2083	Оу
2018 2082	TTACCTCTATCAAGCCAAAAAACTTATCCTCTCCAAGCCCTCTCAAGATCTTGACATAGC	1959 2023	Qу
1958	CATAGAATGGCACAGTGGAGAAAACCCTATCTATTGAAGGCGTTAAAACCTTTGCGCT	1899	Qy
2022		1963	Db
1898	CCGCAACCAATGCTTTTCACAATACTCAAAACGAGTGACATCCAAAACTAACCCAAAAGA	1839	Db
1962		1903	dd
1838	GTTCACTGGAGTGATTGGTGCATTCAACTGCCAAGGAGGAGGATGGTGTCGTGAGACACG	1779	Qy
1902		1843	Db
1778	TTTGTTTGAAGACCCTTTGCATAATGGAGAAACTATGCTTAAGATTTGGAATCTCAACAA	1719	Qy
1842		1783	Db
1718	AGTGCTTCCTGATGGATCGATCCTTCGAAGTGAGTACTATGCACTCCCGACTCGCGATTG	1659	Qy
1782		1723	Db
1658	TGGCCCGATCTATGTTAGTGATTCTGTGGGAAAGCATAACTTTGATCTTCTGAAAAAACT	1599	Qy
1722		1663	Db
1598	TATGTTCCAATCCACCCACCCTTGTGCGCGCCTTCCATGCTGCCTCTCGAGCCATCTCTGG	1539	Qý
1662		1603	da
1538	CATGGTTCATTGTGCCAACGACAGCTTGTGGATGGGGAACTTCATCCACCCTGACTGGGA	1479	Qy
1602		1543	Db
1478	CTTTTGGTGCACGGACCCCTCTGGTGATCCAAACGGTACGTTTTGGCTCCAAGGATGTCA	1419	Qy
1542		1483	Db
1418	TTGTAACGACTTCATGTTCCTTGGCACGGAAGCTATCTCTCTTGGTCGTGTTGGTGATGA	1359	Qy
1482		1423	Db
1358	AATGACCAAATCAATAAATAAACATTTTAAAGGAAATGGAGTCATTGCAAGTATGGAACA	1299	Qy
1422		1363	Db
1298	GGAGATGTTGTGAAGACTATGGAGGGAGAGTGGATTTGGCAAAGGCATATTACAAAGC	1239	Qy
1362		1303	Db
1238	TCATGCTCATTTGGAAAAGTTGGGATCGACGGTGTTAAGATTGACGTTATCCACCTATT	1179	Qy
1302		1243	Db
1242	3 CGTCAGTAACGGAGTTGGACTGGTGCCACCACCCTGGCTCACCTTTTGTACGAGGGGCT	1183	Db

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                               This is the nucleotide sequence of a sugarbeet cDNA clone coding for raffinose synthase (see AN332073), a protein which can bind a D-galactosyl group through an alpha(1-6) bond to the hydroxy group attached to the carbon atom at the 6-position of the D-glucose residue in a sucrose molecule to form raffinose. The cDNA was isolated from sugarbeet cv. haming leaf cDNA by PCR. Probes or PCR primers generated from plant raffinose synthase genes (see AN220207-10) may be used to obtain other raffinose synthase genes may be used to control the levels of raffinose produced in plants. Antisense genes can be used to knock out existing gene activity, and sense genes to increase the level of gene activity. The cresulting transgenic plants may be used as a food source to alter the growing conditions for gut enterobacteria, providing general health advantages. The sense and antisense genes may also be used in gene and phenotypic analysis of plants and for the selection of plants clones with the desired characteristics with respect to
                                                                                                                                                                                                                                                                                                                                                                                                          30-APR-1998;
30-APR-1998;
04-DEC-1998;
                                                                                                                                                                                                                                                                           New sense raffinose
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                                                                                                                                       TTGGGGTGGCCTTCGCCCGCAGGTGCCTGGCCTGAGGCACGTGTGATTCAGCCAGT 1067
                                                                                                                                                                                                   ACTCAAAGGAGAGTTTAAGACTGTGGAGCATGTTTATGTTTTGGCATGCTTTGTGTGGGATA 1007
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              TAAGGTCGGGCTGGTCCCGCCGGAGAAGGCTGAGGAGTGTACGAAGGACTTCATGCTCA 1187
                                                                              GCTTTCACCAGGGCTGCAGATGACGATGGAGGATTTTGGCGGTGGATAAGATTTGTTCA
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                                                                                                                                                                                                                                                  CCCAAATATTATGGGCCATGAGGATCATCCCAATATGGGAATGAGGGCCTTTGTTAGGGA 1182
                                                                                                                                                                                                                                                                              TCCCAAGGCCACCGGCCCCCGAG---CCGGCCAGAAGGGGGATGAAGGCGTTTATAGATGA
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                                                                                                     CATCAGTGAGGATAATGAGGATAAGATGGTTCAGGTTGGTATTAAAGGGGGCCGGAGAAAT
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a mutant protein of raffinose synthation which at least one aromatic amino acid present at the position of about 1-7 amino acids from the N-terminus is deleted or replaced. The mutant protein can be used for reducing the raffinose oligosaccharide content in a plant body. The present polynucleotide from soybean, was used in the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel mutant protein of raffinose synthase is useful raffinose oligosaccharide content in a plant body -
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P-PSDB; AAB98659.
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                                                                                                                                                                                               Vicia faba
                                                                                                                                                                                                                              Raffinose synther gastrointestinal
                                                                                                                                                                                                                                                                         Broad bean raffinose synthetase coding sequence
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                                                                                                                                                                                                                                                                                                                                                                         AAV40800 standard; cDNA to mRNA;
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                  18-DEC-1997;
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                                                                                                                                                                                                                              synthetase; metabolism modification;
estinal flora; broad bean; ss.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence encodes the broad bean raffinose synthetase of the invention. The raffinose synthetase is capable of producing raffinose by combining a D-galactosyl group through an alpha (1-6) bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule. The DNA can be used to modify metabolism of a host organism by introducing into the host organism or its cell so that the content of the raffinose family oligosaccharides in the host organism or cell is changed. Raffinose ollgosaccharides are useful as food additives with beneficial effects on the gastrointestinal flora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid molecule encoding plant raffinose synthetase capable of producing raffinose, used as food additives with beneficial effects on gastrointestinal flora
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 26-29; 44pp; English
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                                               TGTCCTCCCGGTTTAGTCCTAATCGACGATGGTTGGCAATCCATCGGACACGATTCGGAT
                                                                                                                              TACCTAACGGTTCATCCACAGGGCGTAATAGAAGGCGTGAGGCATCTCGTCGACGGCGGT
                                                                                                                                                                                              GAGGAGAAGACTCCACCAGGTATCGTGGACAAATTCGGTTGGTGCACGTGGGACGCGTTT
                                                                                                                                                                                                                                                                                                         AACGACTCCCTCGGACGACCCTATGTCTTACTCCTCCCAATCCTAGAAAACACCTTCCGA
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               CCCATCACCAAAGAAGGAATGAACCAAACCGTCGCCGGCGAGCAAATGCCCTGCCGTCTT
                                                                                                                                                                               GAAGAAAAACAGCACCTAGTATTATAGACAAATTCGGTTGGTGCACGTGGGATGCTTTT
                                                                                                                                                                                                                                             AGTATACTAAAAGAAGCAGTTAAAGTAATCCAAACTCAGTTAGGAACATTCAAGACTCTT
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Pred. No. 3.5e-297;
D; Mismatches 694;
DB 19;
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                                                   GAGTACTATGCACTCCCGACTCGCGATTGTTTGTTTGAAGACCCTTTGCATAATGGAGAA
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                          CGAGTGACATCCAAAACTAACCCAAAAGACATAGAATGGCACAGTGGAGAAAACCCTATC 1929
                                                                            CAAGGAGGAGGATGGTGTGGTGAGACACGCCGCAACCAATGCTTTTCACAATACTCAAAA
                                                                                                       ACTATGCTTAAGATTTGGAATCTCAACAAGTTCACTGGAGTGATTGGTGCATTCAACTGC
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P-PSDB;
              The present sequence encodes a raffinose synthase protein. The sequence is isolated from plant material of broad beans. The protein forms raffinose by complexing alpha(1 to 6). D-galact hydroxyl group of the 6C of D-glucose residue in sucrose mole
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18-DEC-1996;
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2746
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BP;
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96JP-0338673.
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	1150 GAGAAGGCTGAGGAGATGTACGAAGGACTTCATGCTCATTTGGAAAAAGTTGGGATCGAC 1209 	р ₀ у
	1090 ACGATGGAGGATTTGGCGGTGGATAAGATTGTTCTTCATAAGGTCGGGCTGGTCCCGCCG 1149	DЬ
	1030 GTGCCTGGCTTGCCCTGAGGCACGTGTGATTCAGCCAGTGCTTTCACCAGGGCTGCAGATG 1089	р ₆ Оу
	970 GTGGAGCATGTTTATGTTTGGCATGCTTTGTGTGGATATTGGGGTGGCCTTCGCCCGCAG 1029 	P 09
	910 CGAGCCGGCCAGAAGGGGATGAAGGCGTTTATAGATGAACTCAAAGGAGAGTTTAAGACT 969 	p 9
	850 TTGAAATTCCAAGAGAATTACAAATTCCGTGACTAACGTCAATCCCAAGGCCACCGGCCCC 909	Db 09
	790 CCCATCACCAAAGAAGGAATGAACCAAACCGTCGCCGGCGAGCAAATGCCCTGCCGTCTT 849	B 8
	730 TGTCCTCCCGGTTTAGTCCTAATCGACGATGGTTGGCAATCCATCGGACACGATTCGGAT 789 	D 04
	670 TACCTAACGGTTCATCCACAGGGCGTAATAGAAGGCGTGAGGCATCTCGTCGACGGCGGT 729	ρ δ
-	610 GAGGAGAAGACTCCACCAGGTATCGTGGACAAATTCGGTTGGTGCACGTGGGACGCGTTT 669 	D Oy
	550 GCACTTGTTAAAGAGGGGATGAAGATCGTGAAGACCCATCTTGGAACTTTTCGCTTGTTG 609	do Oy
	490 AAAGTTGTTGATGCATCGTTCCGAAGTATGTTGTATCTTCATGCTGGTGATGATCGCTTT 549	D Oy
	430 ACCTCGATTCAGCCTGGGGATGATGACTTTGTCGATGTTTGTGTCGAGAGTGGTTCGTCG 489	Оy
	373 TCAGATTCTGGTCGACCGTATGTTTTCCTTCCGATCGTTGAGGGACCGTTCCGA 429	y dd
	313 TGGGTTGGAAATGGTGGGGATCTTGAATCGGAGACTCAGATTGTGATCCTTGAGAAG 372 	Db Qy
	253 AAGCTGAAGGATATTCGGTTTATGAGGTATTTCAGGTTTAAGGTTTGGTGGACTACACAC 312 	DP 6A
	193 GGTTGCTTTGTTGGATTCGACGCGCGCGCGACCTGATAGCCGACATGTTGTTTCGATTGGG 252 	Ор
ω,	uery Match 40.7%; Score 956.6; DB 20; Length 2746; est Local Similarity 66.6%; Pred. No. 3.5e-297; atches 1421; Conservative 0; Mismatches 694; Indels 18; Gaps	M B Q

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                                                                                                                                                     GTTTCACCAGTGACCAAACTCATCCAAACTTCTCTACACTTTGCCCCAATTGGGCTGGTG
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GTTCAAGTGCCATGGCCAATTGATTCTTCATCG 2322
                   TGCTGCAAAATTGATGGGGGTTAAGGTGAAATTTCTTTATG---AGGACAAAATGGCAAGA 2443
                                       GCTTGTCGTATTGATGGGGAGGATGTTGGGTTCAAGTATGATCAGGACCAAATGGTGGTG
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                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                            The present sequence is a cDNA encoding raffinose synthase from clone sfil.pk125.d4 isolated from a soybean immature flower cDNA library sfil. Raffinose synthase is involved in the biosynthesis of raffinose and higher homologues in the raffinose saccharide family from sucrose. The present sequence is useful for reducing the raffinose saccharide content of soybean seeds which improves the nutritional quality of the soy protein products derived from them.
                                                                                                                                                                                                                                                                                                                                                               Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids and encoded proteins involved in the biosynthesis of raffinose, useful for producing soybean seeds with a reduced raffinose content and therefore improved nutritional quality -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Allen
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TCAGATTCTGGTCGACCGTATGTTTTCCTTCCGATCGTTGAGGGACCGTTCCGAACC
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 AGTCCTAATCGACGATGGTTGGCAATCCATCGGACACGATTCGGATCCCATCACCAAAGA
                                           TCCACAGGGCGTAATAGAAGGCGTGAGGCATCTCGTCGACGGCGGTTGTCCTCCCGGTTTT
                                                                                                                                           CGCCGTGAAGGTGGCGCGCCACCACCTCGGGACGTTCAGGCTGCTGGAGGAGAAAACTCC
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                             GCCCCACGGCGTTATGGAGGGCCTGCAGGGGCTTGGTTGACGGCGGATGTCCGCCGGGGGCT
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/product= raffinose synthetase
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                           GTGTCGTGAGACACGCCGCAACCAATGCTTTTCACAATACTCAAAACGAGTGACATCCAA
                                                       CCCGACTCGCGATTGTTTGTTTGAAGACCCTTTGCATAATGGAGAAACTATGCTTAAGAT
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                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                       Matches 1223;
                                                                                                                                                                                                                                                                                                             The present sequence encodes a raffinose synthase protein. The sequence is isolated from plant material. The protein forms raffinose by complexing alpha(1 to 6)- D-galactosyl hydroxyl group of the 6C of D-glucose residue in sucrose molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 13;
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                                                                                                                                                                                                                                                                   Sequence 1762
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18-DEC-1996;
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DB; AAY30144.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This is the nucleotide sequence of a rapesed cDNA clone coding for raffinose synthase (see AAY32075), a protein which can bind D-galactosyl group through an alpha(1-6) bond to the hydroxy groatched to the carbon atom at the 6-position of the D-glucose residue in a sucrose molecule to form raffinose. The cDNA was isolated from rapesed cv. Westar leaf cDNA by PCR. Probes or
                 1087 ATGACGATGGAGGATTTGGCGGTGGATAAGATTGTTCTTCATAAGGTCGGGCTGGTCCCG
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                                                                  GGAGCTCCTACTCTTCCGCCSTCRACTATTGTCCGRCCAGAGCTCTCGCCGGGGCTTAAG
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                                                                               This is the nucleotide sequence of a soybean cDNA clone coding of raffinose synthase (see AAY3072), a protein which can bind a D-galactosyl group through an alpha[1-6] bond to the hydroxy group attached to the carbon atom at the 6-position of the D-glucose residue in a sucrose molecule to form raffinose. The cDNA was solven for soybean cv. Williams 82 immature seed cDNA by PCR. Probes or primers generated from plant raffinose synthase genes (see AAZ20207-10) may be used to obtain other raffinose synthase genes by labeled detection or amplification (claimed). These genes may be used to control the levels of raffinose produced in plants. Antisense genes to increase the level of gene activity. The and sense genes to increase the level of gene activity. The the growing conditions for gut enterobacteria, providing general chealth advantages. The sense and antisense genes may also be used in gene and phenotypic analysis of plants and for the selection of raffinose content.
 Query Match
Best Local Similarity
Matches 486; Conserv
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK
Tel: 580 221 7391
Fax: 580 221 7380
                                                                                                                                                    Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula drought library Unpublished (2000)
Contact: May GD
                                                                                                                                                                                                                                                                                                    Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Email: gdmay@noble.org
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/dev_stage="Pooled timepoints"
/note="Vector: Lambda Zap; Contains a mixture of entire
plantlets harvested in a series of days-post-watering
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a 125 c 148 g 214 t
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                             TTTATGGATGGGCAACTTTATCCACCCTGATTGGGACATGTTCCAGTCCTCCCACCCTTG
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                                                                {	t TGCTGAGTTCCACGCTTCCAGGGCCCATCTCCGGTGGCCCAATTTACATCANCGACAC}
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brookhaven National Laboratory
Upton, NY 11973, USA
Tel: 516-344-3396
Fax: 516-344-3407
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primer: T3 Primer.
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/Cultivar="Acala Maxxa"
/db_xref="rtaxon:3635"
/clone_lib="Six-day Cotton fiber"
/tissue_type="immature fiber"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="Six days post ant
/nab_host="XLI-Blue"
/nate="Vector: pBluescript II
139 c 149 g 193 t
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GAGATGGTGGGTGAGAAGTATGGTGGAAGAGTTGATTTGGCCAAAGCATATTACAAAGCT
                                                                       CACTCTCTTTTGGAAGAGTCTGGAATTGATGGGGGTCAAGGTTGATGTCATCCATTTGCTA
                                                                                                                                                 GTTAATAATGGTGTTGGGTTAGTTCCTCCTCATTTGGTTGATCAAATGTATGAAGGTATT
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                                                                                                                                                                                                                                                                                                  TGTGGTTATTGGGGTGGGATAAGACCTAATGTTGAGGGTCTACCTGAAGCTATTGTGGAG 61
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Contact: May GD
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BF636478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2510 Sam Noble Parkway, Ardmore,
Tel: 580 221 7391
Fax: 580 221 7380
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The Samuel Roberts Nob
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ert Length: 649 Std Error: 0.00
be: 089 row: A column: 04
primer: TCACACAGGAAACAGCTATGAC.
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Samuel Roberts Noble Foundation
Officery Noble Parkway, Ardmore, OK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Drought"
/tissue_type="Plantlets"
/dev_stage="Pooled timepoints"
/note="Vector: Lambda Zap; Contains a mixture of entiplantlets harvested in a series of days-post-watering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:3880"
/clone="NF089A04DT"
/clone 11th="new"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Alzoaceae; Mesembryanthemum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     616 bp mRNA linear EST 20.
L48-1031T3 Ice plant Lambda Uni-Zap XR expression library,
NaC1 treatment Mesembryanthemum crystallinum cDNA clone L46
                                                                                                                                                                                                                                                                                                                                                               MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Biochemistry University of Nevada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST
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BE131081
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Seq primer: T3
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                                                                                                                                                                                                                                                                                                                                               Email: jcushman@unr.edu
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                 177
                 ß
          /dev_stage="Six week old"
/note="Vector: Lambda Uni-Zap
EcoRI; Site_2: XhoI"
133 c 144 g 162 t
                                                                                /clone_lib="Ice plant Lambda Uni-Zap xR
, 48 hours NaCl treatment"
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                                                                                                                                     /organism="Mesembryanthemum crystallinum"
/db_xref="taxon:3544"
/clone="L48-1031"
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458; Conser
                                          Brookhaven National Laboratory
Upton, NY 11973, USA
Tel: 516-344-3396
                                                                                                                                                                                                                                                     AI727581 Six-day Cotton fiber Gossypium hirsutum cDNA to (AF073744) raffinose synthase [Cucumis sativus], mRN/ AI727581 GI:5046433
 Fax: 516-344-3407
Email: burr@bnlux:
Seq primer: T3 Pr:
                                                                                       Biology Department
                                                                                                      Contact: Ben Burr
                                                                                                                     Unpublished (1999)
                                                                                                                                                   Blewitt, M., Matz, E.C.,
                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
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               burr@bnlux1.bnl.gov
      T3 Primer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAGAGTTGATCTTGCAAAAGCTTATTATAAAAGCTTTAACAGATTCAGTTAAAAAAGCATT
                                                                                                                                                                                         NF061C04DT1F1033 Drought 5', mRNA sequence. BF634464
                                                    Medicago.

1 (bases 1 to 682)
                                                                                  Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzale Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D. Expressed Sequence Tays from the Samuel Roberts Medicago truncatula drought library
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/dev_stage="Six days post anthesis"
/lab_host="XLI-Blue"
/note="Vector: pBluescript II KS+"
96 c 129 g 156 t
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/clone_lib="Six-day Cotton
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GTGCAAGTTGGAATTAGAGGTGCTGGTGAGATGAGGGGGTCTATGCTTCANAGAAACCAAG
                             GTCGAGATTGGTGTCAAAGGGTGTGGTGAGATG-CGAGTATTTGCATCGAAAAAACCAAG
                                                                                              AACATGCTTAACACTAGTGGAGCCATCCAATCTGTGGACTATGACGATGACCTAAGCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
73402,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: gdmay@noble.org
Insert Length: 682 Std Error: 0.0
Plate: 061 row: C column: 04
Seq primer: TCACACAGGAAACAGCTATGAC.
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Contact: May GD
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/db_xref="taxon:3880"
/clone="NF061C04DT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="Plantlets"
/dev_stage="Pooled timepoints"
/note="Vector: Lambda Zap; Con
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  TTTTGGCTACAAGGGTGTCACATGGTGCATTGTGCATACAACAGCTTGTGGATGGGCAAT 61
                                                                                                      409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sai72bl0.yl Gm-c1068
ID: Gm-c1068-3932 5'
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Public Soybean EST Project
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoldeae; Phaseoleae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available through: ResGen, Invitrogen Corp. South Memorial Parkway Huntsville, AL 35001 For further in call: (800)-533-3363 or contact via email: ccu@resgen.com High quality sequence stop: 423.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
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Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4444 Forest Park Parkway, Box 8501,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      greenhouse grown"
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/db_xref="taxon:3847"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="GENOME SYSTEMS CLONE ID: Gm-c1068-3932"
/clone_lib="Gm-c1068"
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                                                                                                    0;
                                                                                                                            Score 322;
Pred. No. 7
                                                                                                      Mismatches
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                                                                                                                                                  Contact: Wing RA
Clemson University Genomics
Clemson University
100 Jordan Hall, Clemson, SC
Tel: 864 656 7288
                                                                                              Seq |
High
                                                                                                                                                                                                                                                 Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T.,
,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, develop
                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
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boreum cDNA clone GA__Eb0005F08f, mRNA
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quality sequence stop: 563.
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864 656 4293
                                                                                                                         rwing@clemson.edu
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/db_xref="taxon:29729"
/clone="GA__Eb0005F08f"
                          /cultivar="8400"
                                        /organism="Gossypium
/strain="AKA"
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REFERENCE

Glycine

(bases 1 to 560)

AUTHORS

Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,

Beck,C

Khanna

Eukaryota; Viridiplantae: Streptophyta; Embry Spermatophyta; Magnoliophyta; eudicotyledons; Rosidae; eurosids I; Fabales; Fabaceae; Papil

Embryophyta; Tracheophyta; Papilionoideae; Phaseoleae

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                                                                   BM887415 560 bp mRNA linear EST 08-MAR-2002 sam38b08.yl Gm-c1068 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1068-6976 5' similar to TR:Q9ZT62 Q9ZT62 RAFFINOSE SYNTHASE ;,
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/note="Vector: pBK-CMV; Site_1:
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                 AATACTCAAAACGAGTGACATCCAAAAACTAACCCAAAAGACATAGAATGGCACAGTGGAG
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Tel:
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This clone is available through: ResGen, Invitrogen Corp.
South Memorial Parkway Huntsville, AL 35801 For further in
call: (800)-533-4363 or contact: ccu@resgen.com web site:
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St.
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High quality sequence stop:
Location/Qualifiers
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Contact: Shoemaker R/Public Soybean
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from mRNA isolated from drought stressed leaf tissue of the cultivar Williams 82. The month old greenhouse grown plants were deprived of water for 3 days prior to harvesting the stressed leaf tissue. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a xhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the ligated cDNA fragments were directionally cloned into the ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Soybean EST Project
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/clone_lib="Gm-c1068"
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/db_xref="taxon:3847"
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Pred. No. 9.4
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Gm-c1068-6976"
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CAAAGTTGGGAGTCACAACTTTGAACTCCTCAAGACTTTGGTCTTGCCTGATGGGTGCAT
                                                                                                        TTCTGTGGGAAAGCATAACTTTGATCTTCTGAAAAAACTAGTGCTTCCTGATGGATCGAT 1679
                                                                                                                                                                                   TTGTGCCGCCTTCCATGCTGCCTCTCGAGCCATCTCTGGTGGCCCGATCTATGTTAGTGA 1619
                                                                                                                                                                                                                                                                                                                                                                         TGGTGACCCAAATGGCACATTTTGGCTGCAAGGGTGTCACATGGTGCACTGTGCCTACAA 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Asamizu.E., Nakamura.Y., Sato,S. and Tabata,S. Generation of 7137 non-redundant expressed seq legume, Lotus japonicus
DNA Res. 7 (2), 127-130 (2000)
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/clone_lib="Lotus japonicus young plants (
/clone_lib="Lotus japonicus young plants (
/dev_Stage="young plants (two-week old)"
/dev_Stage="young plants (two-week old)"
/note="Vector: pBbluescriptII SK-; Site_1:
/note="Vector: pBbluescriptII SK-; Site_1:
xhoI; isolate=Miyakojima MG-20"

117 c 119 g 129 t
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/db_xref="taxon:34305"
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Pred. No. 4.6e-76;
0; Mismatches 119;
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CAGCCAGTGCTTTCACCAGGGCTGCAGATGACGATGGAGGATTTGGCCGGTGGATAAGATT 1119
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                              TGTGGTTATTGGGGTTGGGATAAGACCTAATGTTGAGGGTCTACCTGAAGCTATTGTGGAG
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BF636592
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The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
OK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
                                                                                                                                                                                                                                                                                                                                                                                          2510 Sam Noble Parkway, Ardmore,
Tel: 580 221 7391
Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: May GD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Torrez-Jerez, I., Scott, A.D., Harris, A.R., Gonzale Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D. Expressed Sequence Tays from the Samuel Roberts N Medicago truncatula drought library
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                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                  il: gdmay@noble.org
ert Length: 513 Std Error: 0.0
te: 090 row: H column: 02
primer: TCACACAGGAAACAGCTATGAC
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                                                                                       Conservative
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72 c
                                                                                                                                                                                        plantlets harvested in a series of
                                                                                                                                                                                                    /tissue_type="Plantlets"
/dev_stage="Pooled timepoints"
/note="Vector: Lambda Zap; Contains a mixture of entire
                                                                                                                                                                                                                                                             /db_xref="taxon:3880"
/clone="NF090H02DT"
                                                                                                                                                                                                                                              /clone_lib="Drought"
                                                                                                                                                                                                                                                                                           /organism="Medicago truncatula"
                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
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                                                                                    Score 293.4; DB 12;
Pred. No. 2.1e-75;
0; Mismatches 137;
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                                                                                                                                                                                                    Tel: (613) 759-1662
Fax: (613) 759-1701
Email: singhja@em.agr.ca.
Location/Qualifiers
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Singh, J.A., Wakui, K., Couroux, P., De Moors, A., Harris, L.J.,
J.I., Ouellet, T., Robert, L.S., Sprott, D. and Tinker, N.A.
Expressed Sequence Tags from Cold-Stressed Maize Seedlings
Unpublished (2001)
Contact: Singh, J.A.
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BG321136 GI:13150814
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                              /tissue_type="Leaf, crown"
/note="Vector: Bluescript SK-/XhoI-EcoRI; Site_1: Eco RI; Site_2: Xho I; Lower temperature 50 C / hour from 22 to 120C; bring to 50 in 1 hour from 120C. Leave at 50C 2 days photoperiod 16 hours. Light intensity was 125 uE-1. Library prepared by in vivo mass excision from amplified library."
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                                                                                              BM886707 528 bp mRNA linear EST 08-MAR-2002 sam29b05.yl Gm-c1068 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1068-6201 5' similar to TR:Q9ZT62 Q9ZT62 RAFFINOSE SYNTHASE ;,
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Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.
Wylle,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 38801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
Tel: 314 286 1800
Fax: 314 286 1810
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Contact: Shoemaker R/Public
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from mRNA isolated from drought stressed leaf tissue of the cultivar Williams 82. The month old greenhouse grown plants were deprived of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 greenhouse grown"
/lab_host="DH10B"
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/clone_lib="Gm-cl068"
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                                                                                                                                                                                                                                                                                                                      This clone is available through: ResGen, Invitrogen Corp. South Memorial Parkway Huntsville, AL 35801 For further in call: (800)-533-4363 or contact via email: ccu@resgen.com Insert Length: 1160 Std Error: 0.00
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82. The month old greenhouse grown plants were deprived water for 3 days prior to harvesting the stressed leaf tissue. Complementary DNA was synthesized from mRNA usir a primer consisting of a poly(dT) sequence with a XhoI
                                                                        /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed from mRNA isolated
from drought stressed leaf tissue of the cultivar Williams
                                                                                                                                                    /tissue_type="Leaf, drought stressed, 1 month old greenhouse grown"
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/db_xref="taxon:3847"
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AAGACCCTTTGCATAATGGAGAAACTATGCTTAAGATTTGGAATCTCAACAAGTTCACTG 1786
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                                                 Chen, J., Momiyama, M., Chan, E., Mooney, M., Carroon, B., Gillila Wang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P. Gorgone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D., Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C., Carpio, Policky, J., Suzuki, G., Argentine, C., Shah, S., Nobriga, A., Mur Turner, C., Krikorian, S., Elder, L. and Hanson, D.
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701496022 A. thaliana, Ohio State clone set
cDNA clone 701496022, mRNA sequence.
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Arabidopsis thaliana Gene Expression MicroArray Unpublished (1999)
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AI993310.1
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Best Local Similarity 69.0%;
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Genome Systems, Inc., a wholly owned subsidiary of Incyte Pharmaceuticals, Inc.
4633 World Parkway Circle, St. Louis, MO 63134, USA
Tel: 877-577-2733
Fax: 314-427-3324
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/db_xref="taxon:3702"
/clone="701496022"
/clone=11b="A. thaliana, Ohio State clone set"
/clone_cona library was made from selected clones from the Arabidopsis thaliana Ohio State clone set."
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TOPOLOGY: Linear MOLECULE TYPE: cDNA to mRNA ORIGINAL SOURCE: ORGANISM: cucumber (Cucumis sativas) FEATURE: NAME/KEY: CDS LOCATION: 562407 US-08-846-234-4 OHERY MATCH	APPLICATION NUMBER: U5/08/846,234 FILING DATE: ATTORNEY/AGENT INFORMATION: NAME: NORMAN F. OBLON REGISTRATION NUMBER: 24,618 FELECOMMUNICATION INFORMATION: TELEPHONE: (703)-413-3000 TELEFAX: (703)-413-2220 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 2517 base pairs TYPE: nucleic acid	S O, Version #1.	NTHASE GENE, FFINOSE, AND ELLAND, MAIE S HIGHWAY, F	RESULT 1 US-08-846-234-4 Sequence 4. Application US/08846234	C 28 33.6 1.4 4377 4 US-09-479-453-28 US-08-971-188-1 30 33.4 1.4 1505 1 US-079-915-246-1 31 33.4 1.4 16442 3 US-08-979-542-101 C 31 33.4 1.4 2561 4 US-08-970-542-101 C 33 33 1.4 2561 4 US-09-270-542-119 C 34 33 1.4 34303 2 US-08-735-609-4 C 35 33 1.4 34303 3 US-09-244-752-4 C 36 33 1.4 34303 3 US-09-244-752-4 C 38 33 1.4 34303 3 US-09-244-752-4 C 38 33 1.4 34303 3 US-09-245-497-4 US-08-735-609-1 C 40 33 1.4 34303 3 US-09-245-497-4 US-08-562-919-4 US-08-563-669-3 C 43 33 1.4 34303 4 US-09-245-497-4 US-08-563-669-3 C 43 33 1.4 35408 4 US-08-563-669-3 C 44 33 1.4 35408 4 US-08-563-669-3 C 44 33 1.4 35408 4 US-08-549-489-3 C 44 33 1.4 35408 4 US-08-549-489-3 US-08-
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Matches 2352;

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1135	76 CGCCCGCAGGTGCCTGGCTTGCCTGAGGCACGTGTGATTCAGCCAGTGCTTTCACCAGC	Db 10
1080	21 CGCCCGCAGGTGCCTGGCCTGAGGCACGTGTGATTCAGCCAGTGCTTTCACCAGGG	Оу 10
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1020	61 TTTAAGACTGTGGAGCATGTTTATGTTTGGCATGCTTTGTGTGGATATTGGGGTGGCC1	Оу 9
960 1015	01 ACCGGCCCCCGAGCCGGCCAGAAGGGGATGAAGGCGTTTATAGATGAACTCAAAGGAGAG	Qy 9 Db 9
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0	41 TGCCGTCTTTTGAAATTCCAAGAGAATTACAAATTCCGTGACTACGTCAATCCCAAGGCC	œ
895	1 GATTCGGATCCCATCACCAAAGAAGGAATGAACCAAACCGTCGGCGGGGAGCAAATGCCC 1	Db 49
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780	'21 GACGGCGGTTGTCCTCCCGGTTTAGTCCTAATCGACGATGGTTGGCAATCCATCGGACAC	0y 7
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715	56 CGCTTGTTGGAGGAGACTCCACCAGGTATCGTGGACAAATTCGGTTGGACGTGG	Db 6
660	01 CGCTTGTTGGAGGAGAAGACTCCACCAGGTATCGTGGACAAATTCGGTTGGTGCACGTGG	Оу б
	96 GATCCGTTTGCACTTGTTAAAGAGGCGATGAAGATCGTGAGGACCCATCTTGGAACTTTT	
600	41 GATCCGTTTGCACTTGTTAAAGAGGCGATGAAGATCGTGAGGACCCCATCTTGGAACTTTT	0у 5
540 595	81 GGTTCGTCGAAAGTTGTTGATGCATCGTTCCGAAGTATGTGTATCTTCATGCTGATGATGTTGATGCTGATGATGTTCGTATGTTGATGCTGATGATGATGTTGTATCTTCATGCTGATGATGTTGTATCTTCATGCTGATGTGATGTTGTATCTTCATGCTTGATGTGTATGTA	Qy 4 Db 5
	.76 CCGTTCCGAACCTCGATTCAGCCTGGGGATGATGTTTGTT	4
480	21 CCGTTCCGAACCTCGATTCAGCCTGGGGATGATGACTTTGTCGATGTTTGTGTCGAGAGT	0у 4
475	16 ATCCTTGAGAAGTCAGATTCTGGTCGACCGTATGTTTTCCTTCTTCCGATCGTTGAGGGA	Db 4
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300	TTTCGATTGGGAAGCTGAAGGATATTCGGTTTATGAGTATTTTCAGGTTTAAGGTTTGG	Qy 2
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180	CCGATGTTCCTGAGAACATTGTTGCTTCTCCTTCTCCGTACACTTCGATAGACAAGTCC	Qy 1
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APPLICANT: ISHIGE, Fumiharu
APPLICANT: WATANABE, E111ro
APPLICANT: OEDA, Kenji
TITLE OF INVENTION: PLANT PROMOTERS
FILE REFERENCE: 2185-0431P
CURRENT APPLICATION NUMBER: US/09/561,825
CURRENT FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: JP 11-124527
PRIOR APPLICATION NUMBER: JP 11-124527
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: JP 11-247211
PRIOR FILING DATE: 1999-09-01
SEQ ID NO 23
SEQ ID NOS: 30
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Best Local Similarity 66.0%;
Matches 1507; Conservative
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LOCATION: (62)..(2407)
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TYPE: DNA
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FEATURE:
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Patent No. 5670367
GENERAL INFORMATION:
CIT.
STATE: VA
COUNTRY: USA
TD: 22313-0299
                                                                                                                                 APPLICANT: DORNER, F.
APPLICANT: SCHEITLINGER, F.
APPLICANT: FALKWER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                        2380
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US-08-232-463-14
                                                                                                                                                                                               US-09-457-046B-19
                                                                                                                                                                                                                 RESULT 4
                   GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: Transacylases of the PR
FILE REFERENCE: 53679
CURRENT APPLICATION NUMBER: US/09/457,046B
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEO ID NOS: 74
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                         Sequence 19, Application US/09457046B Patent No. 6287835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.0%; Score 47.4; DB 1; Best Local Similarity 4.7%; Pred. No. 0.00024; Matches 15; Conservative 178; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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IMMEDIATE SOURCE:
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TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: TBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
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NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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                                                                                                                                                                                                                                                                   CCCTCGACCTGCAGCCA 1040
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                                                                                                                                                                                                                                                                                                    CCTTGGCACGGAAGCTA 1393
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linear
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                                                                                                        Transacylases of the Paclitaxel Biosynthetic
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Length

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Gaps

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APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
FILE REFERENCE: 53679
CURRENT APPLICATION NUMBER: US/09/457,046B
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21
LENGTH: 911
TYPE: DNA
ORGANISM: Taxus cuspidata
US-09-457-046B-21
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US-09-457-046B-21
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; ORGANISM: Taxus cuspidata
US-09-457-046B-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21, Application US/09457046B Patent No. 6287835 GENERAL INFORMATION:
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LENGTH: 911
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Best Local Similarity 47.2%;
Matches 116; Conservative
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Best Local S
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Local Similarity 47.2%;
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ATAATG 706
                                   TTAAAG 562
                                                                                             TTGATGCATCGTTCCGAAGTATGTTGTATCCTTCATGCTGGTGATCATCCGTTTGCACTTG 556
                                                                                                                                                                                                                                                                                                TTGTTATAAATGTTGACACCATAGAATATATGAAACAATGTGTTATGGAGGAATGTAATG 520
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                                                                                                                                              TTCAAATTCCACATACTGAGAATGTGAAGCTTCTCTTTGCGATGGATTTGAGGAAATTAT 640
                                                                                                                                                                               TTCAGCCTGGGGATGATGACTTTGTCGATGTTTGTCTCGAGAGTGGTTCGTCGAAAGTTG 496
                                                                                                                                                                                                                      ATTTTTGTTCGTCCTTTGAAGTAGTGGCAGCATTGGTTTGGATAGCAAGGACAAAGGCTC 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGATGCATCGTTCCGAAGTATGTTGTATCTTCATGCTGGTGATGATCCGTTTGCACTTG 556
                                                                                                                                                                                                                                                           ATTCTGGTCGACCGTATGTTTTCCTTCCTTCCGATCGTTGAGGGACCGTTCCGAACCTCGA 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTTTTGTTCGTCCTTTGAAGTAGTGGCAGCATTGGTTTGGATAGCAAGGACAAAGGCTC 580
                                                                                                                                                                                                                                                                                                                                                                                         Score 38; DB 4; Length 911; Pred. No. 0.065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38; DB 4; Length 911.
Pred. No. 0.065;
                                                                                                                                                                                                                                                                                                                                                                        Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                        Indels
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RESULT 7
US-09-010-928B-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: YE, Jane et al
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE
TITLE OF INVENTION: NUCLEIC ACID MOLECULES
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL001058
CURRENT APPLICATION NUMBER: US/09/740,035
CURRENT FILING DATE: 2000-12-20
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-740-035-3/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09740035 Patent No. 6344353 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Applic Patent No. 5994099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                          ATTORNEY/AGENT INFORMATION:
NAME: MUTDBY JT., Gerald M
REGISTRATION NUMBER: 28977
REFERENCE/DOCKET NUMBER: 14
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 19736
TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF ENCUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART,
ADDRESSEE: ATTO GATEHOUSE RD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1809 CCAAGGAGGATGGTGTCGTGAGACACGCCGCAACCAATGCTTTTCACAATACTCAAA 1868
                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                    SEQUENCE CHARACTERISTICS:
LENGTH: 2824 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lewis, Randolph V
APPLICANT: Hayyashi, Cheryl Y
TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA
TITLE OF INVENTION: CODING THEREFOR
                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
ZIP: 220
                                                                                                                                                                          APPLICATION NUMBER: US/09/010,928B FILING DATE: 22-JAN-1998 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 8110 GATEHO
CITY: FALLS CHURCH
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.6%;
Local Similarity 53.5%;
les 77; Conservation
STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                     22042
                   nucleic acid
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                                    2824 base pairs
                                                                                                                                                                                                                                                                                                                                                                                        UNITED STATES
not relevant
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ISOLATED HUMAN PROTEASE PROTEINS,
NUCLEIC ACID MOLECULES ENCODING
USES THEREOF
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                                                                                                    1447-109P
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Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  KOLASCH & BIRCH
SUITE 500E
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                                                                                                                                                                                                                                                                   Version
                                                                                                                                                                                                                                                                   #1
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US-09-383-630-4/c

(Sequence 4, Application US/09383630A; Patent No. 6265632;

(GENERAL INFORMATION:
APPLICANT: AVNET Yayon et al.
APPLICANT: AVNET YAYON ET ANTIAL ATTIAL ATTIAL RE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                     TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1038 TTCCGGAGGACCCGGTGGTGCTGGCGGA 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1145 CGCCGGAGAAGGCTGAGGAGATGTACGA 1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1085 AGATGACGATGGAGGATTTGGCGGTGGATAAGATTGTTCTTCATAAGGTCGGGCCTGGTCC 1144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
COMPUTER: MS DOS Version 6.2,
OPERATING SYSTEM: MS DOS Version 3.11
Windows version 2.0 cor
                                                                                                    REGISTRATION NUMBER: 33,8
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
                                                                                                                                                                                                                                                                                                                                     to an ASCI file CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 18 CORRESPONDENCE ADDRESS:
                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                    APPLICATION NUMBER: <Unknown>
                                                                                                                                                                                                                                                                                 FILING DATE: 26-Aug-1999 CLASSIFICATION: <Unknown>
                                                                             TELEPHONE: 972-3-562554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 2001 Je
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Mark M. Friedman c/o Anthony Castorina STREET: 2001 Jefferson Davis Highway, Suite 207
                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/383,630A
                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Word for Windows version 2.0 converted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: United States of America
                                                                                                                                                                                     NAME:
LENGTH: 8083
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                                                                                                                                                                               Friedmam, Mark M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA
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taken from 3' region. Stop codon begins at position 2722."
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                                                                                                                                                              33,883
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                                                                                                                                           1402/2
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RESULT 9
US-09-383-630-5/c
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                                                                                US-09-383-630-5
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GENERAL INFORMATION:
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Best Local Similarity
Matches 87; Conserv
                                    Query Match
Best Local Similarity Matches 87; Conserv
                                                                                                                                                                                                                       TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4857 AAGGGTTACTGTCTCCCACACTAAGCACCACCAGGGGCTTGCCTCACCAAG 4806
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          742 TTAGTCCTAATCGACGATGGTTGGCAATCCATCGGACACGATTCGGATCCCATCACCAAA 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Word for Windows version to an ASCI file CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/383,630A FILING DATE: 26-Aug-199 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 972-3-5625553
                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                    SEQUENCE DESCRIPTION: SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Avner Yayon et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAGGAATGAACCAAACCGTCGCCGGCGAGCAAATGCCCTGCCGTCTTTTGAAATTCCAA 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAAACCCTGGACTACTGCGCCCGGGGGATCTGCAGCCCGGGGGATCCACTAAGATCCCCT 4858
                                                                                                                                   STRANDEDNESS: double
                                                                                                                                                              TYPE: nucleic acid
                                                                                                                                                                                LENGTH: 8083
                                                                                                                                                                                                                                                              TELEFAX: 972-3-5625554
                                                                                                                                                                                                                                                                                                                                          NAME: Friedmam, Mark M. REGISTRATION NUMBER: 33,883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: MS DOS version 6.2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: United States of America
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STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Mark M. Friedman c/o Anthony Castorina STREET: 2001 Jefferson Davis Highway, Suite 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
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                  1.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Windows version 3
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Score 36; DB Pred. No. 1.3; 0; Mismatches
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                                         DB 4; Length 8083;
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Query Match
Best Local Similarity
Trahes 77; Conserv
                                                                                                                                                        : NAME/KEY: CDS
; LOCATION: 183..2675
; OTHER INFORMATION: /product- "N. clavipes minor
; OTHER INFORMATION: ampullate silk protein"
US-08-209-747-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/209
FILING DATE: 14-MAR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MUTCHY JI., Gerald M.
REGISTRATION NUMBER: 28,977
REGISTRATION NUMBER: 1447
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2793 base pairs
                                  1029 GCTGCCTGGCTTGCCTGAGGCACGTGTGATTCAGCCAGTGCTTTCACCAGGGCTGCAGAT 1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICANT: Colgin, Mark
TITLE OF INVENTION: cDNAs Encoding Minor Ampullate Spider
TITLE OF INVENTION: Silk Proteins
                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STREET: P.O. Box 747
CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: doub
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                                                                                                                                                                                                                                                                                     ORGANISM: Nephila clavipes
TISSUE TYPE: minor ampullate gland
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GGTGCCGGAGCAGGAGCTGCTGCTGCTGCTGCTGCAGGAGCAGGAGGTGCTGGT 1738
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                                                                                              Score 35.6; DB Pred. No. 0.84;
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INFORMATION FOR SEQ ID NO:
                                    1679
1089 GACGATGGAGGATTTGGCGGTGGATAAGATTGTTCTTCATAAGGTCGGGCTGGTCCCGCC 1148
                                                                      1029 GGTGCCTGGCTTGCCTGAGGCACGTGTGATTCAGCCAGTGCTTTCACCAGGGCTGCAGAT 1088
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
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APPLICATION NUMBER: US
FILING DATE: 02-JUN-19
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: cDNAs Encoding Minor Ampullate Spider TITLE OF INVENTION: Silk Proteins
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                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
ORGANISM: Nephila clavipes
                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CI
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: 183..2675
OTHER INFORMATION: 6
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                          TISSUE TYPE: minor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Murphy Jr., Gerald M. REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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                                     GGTGCCGGAGCAGGAGCTGGTGCGGCTGCTGCTGCTGCAGGAGCAGGAGGTGCTGGT 1738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22040-3487
                                                                                                                                                                                                                                                                                                                                                                                                                : 2793 base pairs
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                                                                                                            Conservative
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O. Box 747
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                                                                                                                             1.5%;
52.7%;
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                                                                                                                             Score 35.6; DB 1; Pred. No. 0.84;
                                                                                                            Mismatches
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                                                                                                            Indels
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TACGGTAGAGGTGCTGGAGCTGGAGCTGCAGGTGCTGGAGCTGGAGCCGCT 1798

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; PAGES: 7120-7124
; DATE: Sept.-1990
; RELEVANT RESIDUES
US-08-425-069-1
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US-08-425-069-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 28,977
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEPAX: 7703)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Xu, Ming
APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 6
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                                                                                                                                                                                                                                                 PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                               LOCATION: 1..2154
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                            TITLE: Structure of a protein superfiber: TITLE: drafline silk
                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Birch, Stewart, Kolasch & Birch STREET: 301 No. 5728810th Washington Street CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/425,069 FILING DATE: 19-APR-1995 CLASSIFICATION: 435
                                                                                                                                                                                                             AUTHORS: Xu, Ming
AUTHORS: Lewis, Randolph V.
                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Nephilia clavipes
                                                                                                                                                            JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
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 Similarity 49.0
94; Conservative
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Score 35.2; [Pred. No. 1; 0; Mismatches
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08317844B Patent No. 5989894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     TELEFAX: (703) 241-284
TELEX: 248345
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:

NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 241-1300
                                              NAME/KEY: CDS
LOCATION: 1..2154
OTHER INFORMATION: /pro
OTHER INFORMATION: drag
PUBLICATION INFORMATION:
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APPLICANT:
                                                                                                                                                                     ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                    FEATURE:
                                                                                                                                                                                   TUPOLOLI TYPE: CD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1461 ACGAGGTGGACA 1472
                 AUTHORS:
                                                                                                                                                   ORGANISM:
                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                       TELEPHONE: (703) 241-2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 04-OCT CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Birch, Stewart, Kolasch & Birch STREET: 301 No. 5989894th Washington Street CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
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Y: U.S.A.
Structure of a
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               Lewis, Randolph V.
                                 Xu, Ming
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Xu, Ming
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                                                                                   /product=
                                                                dragline
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protein superfiber:
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                                                                silk protein"
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 Spider
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VOLUME:

drafline silk
Proc. Natl. Acad. Sci. U.S.A.

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CURRENT APPLICATION NUMBER: US/09/457,046B; CURRENT FILING DATE: 1999-12-07; NUMBER OF SEQ ID NOS: 74; SOFTWARE: PATENTIN Ver. 2.1; SEQ ID NO 53; LENGTH: 1326; TYPE: DATE ORGANISM: Taxus cuspidata
US-09-457-046B-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAGES: 7120-7124
DATE: Sept.-1990
RELEVANT RESIDUES IN SEQ ID NO:
US-08-317-8448-1
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US-09-457-0468-53
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Patent No. 6287835
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
FILE REFERENCE: 53679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.9
Best Local Similarity 49.0
Matches 94; Conservative
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Best Local Similarity
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                                   557 TTAAAG 562
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                                                                                                                                                                                                                                                                                                                               317 TTGGTCGAAATGGTGGGGATCTTGAATCGGAGACTCAGATTGTGATCCTTGAGAAGTCAG 376
 926
                                                                                                                                                                                                                          746 AATTTTGTTCGTCTTTTGAAGTAGTGGCAGCATTGGTTTGGATAGCACGGACAAAGGCTC 805
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ATAATG 931
                                                                        TTAATCCCCCACTTCCAAATGGATATTATGGTAATGCCATTGGTACTGCATATGCAATGG
                                                                                                            TTGATGCATCGTTCCGAAGTATGTTGTATCTTCATGCTGGTGATGATCCGTTTGCACTTG 556
                                                                                                                                                 TTCAAATTCCACATACTGAGAATGTGAAGCTTCTCTTTGCGATGGATTTGAGGAAATTAT 865
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Pred. No. 1;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 18596
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Johnson, William G.
APPLICANT: Stenroos, Edward S.
APPLICANT: Stenroos, Edward S.
TITLE OF INVENTION: METHODS FOR DIAGNOSING,
TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
FILE REFERENCE: 601-1-057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/09318448 Patent No. 6210950
                                                                                                                                                                                                                                               Matches
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NUMBER OF SEQ ID NOS: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/318,448
                                                                                                                                                            5157 CCTGGGAGGTGCGGTGAGCCACGATCGCGCCATTGCACTCCAGCCTGGGCAAC 5216
                                                                               5217 AAGAGCGAAACTCTCAAAAAACAAAAAAAAGGATGGGTTCCATATGGGTG 5266
                                                                                                                   1869 ACGAGTGACATCCAAAACTAACCCAAAAGACATAGAATGGCACAGTGGAG 1918
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Local Similarity 57.3%;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                  Published_Applications_NA:*

1: /cgn2_6/ptodata/2/pubpna/P

2: /cgn2_6/ptodata/2/pubpna/U

3: /cgn2_6/ptodata/2/pubpna/U

4: /cgn2_6/ptodata/2/pubpna/U

6: /cgn2_6/ptodata/2/pubpna/U

5: /cgn2_6/ptodata/2/pubpna/U

6: /cgn2_6/ptodata/2/pubpna/U

9: /cgn2_6/ptodata/2/pubpna/U

10: /cgn2_6/ptodata/2/pubpna/U

11: /cgn2_6/ptodata/2/pubpna/U

12: /cgn2_6/ptodata/2/pubpna/U

13: /cgn2_6/ptodata/2/pubpna/U

14: /cgn2_6/ptodata/2/pubpna/U

15: /cgn2_6/ptodata/2/pubpna/U
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2352
1 ATGGCTCCTAGTTTTAAAAA
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8318.946 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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16 17 18 19	111111 15432109876543	2	NO t
37 37 36.8	75.4 44.4 44.4 38 38 37.3 37.4 37.4 37.4	113.2	Score
1.666		4.8	Query Match
5222 5696 5757 750	296 377 160 911 911 46050 1664 1664 1664	1036	Query Match Length
100	000000000000000000000000000000000000000	10	DB
US-09-993-170-57 US-09-993-170-60 US-09-993-170-56 US-10-184-644-104	US-09-294-093B-2999 US-09-878-574-1840 US-09-878-574-1940 US-09-866-570A-19 US-09-866-572A-21 US-09-866-572A-21 US-09-866-572A-21 US-09-860-572A-21 US-09-860-572A-21 US-09-820-003A-3 US-10-091-504-1272 US-09-764-869-1272 US-09-764-869-1272 US-09-764-869-1272 US-09-764-869-1272	US-09-770-445-180 US-09-878-574-2803	ID
Sequence 57, Appl Sequence 60, Appl Sequence 56, Appl Sequence 104, App		Sequence 180, App Sequence 2803, Ap	Description

Query Match 4.8%; Best Local Similarity 62.9%; Matches 175; Conservative (

Score 113.2; DB 10; Length 1036; Pred. No. 6.2e-25; 0; Mismatches 103; Indels 0;

Gaps

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33.8	34	34	34	34.2	34.2	34.6	34.8	34.8	34.8	34.8	34.8	34.8	34.8	34.8	ω U	35	35	35	35	35.2	35.4	35.4	36	36.2	
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US-09-815-242-7419	US-10-263-788-1	US-09-070-927A-129	US-09-815-242-6833	US-09-764-847-1426	US-10-092-154-1426	JS-09-901-136-3	US-09-967-768A-119	US-09-880-107-1590	JS-09-954-531-348	JS-09-954-531-124	US-09-866-572A-53	US-09-866-570A-53	JS-10-184-644-346	US-09-867-701-6593	US-09-816-093-3	JS-10-274-873-3	US-09-764-847-1680	US-10-092-154-1680	JS-10-025-380-1125	JS-10-184-644-402	JS-10-071-766-85	US-09-822-846-199	US-09-811-825-3	US-09-864-761-11473	
Sequence 7419, Ap	Sequence 1, Appli	Sequence 129, App	Sequence 6833, Ap	Sequence 1426, Ap	Sequence 1426, Ap	Sequence 3, Appli	Sequence 119, App	Sequence 1590, Ap	Sequence 348, App	Sequence 124, App	Sequence 53, Appl	Sequence 53, Appl	Sequence 346, App	Sequence 6593, Ap	Sequence 3, Appl.	Sequence 3, Appli	Sequence 1680, Ap	Sequence 1680, Ap	Sequence 1125, Ap	Sequence 402, App	Sequence 85, Appl	Sequence 199, App	Sequence 3, Appli	Sequence 11473, A	and dry on a second

ALIGNMENTS

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; LENGTH: 1036
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-445-180
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US-09-770-445-180/c
                                                               SOFTWARE: FOR SEQ ID NO 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 180, Application US/09770445 Patent No. US20020023281A1
                                                                                                              APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2023US (PARA-012PRV)
CURRENT APPLICATION NUMBER: US/09/770,445
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178,472
                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                         PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 2000-01-27
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                                                                                             NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                      Matthew, Abraham V.
Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
                                                                            FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                    Hoffman, Neil
Hurban, Patrick
                                                                                                                                                                                                                                                         Davis, Keith R. Allen, Keith
                                                                                                                                                                                                                                                                                       Slader,
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Slader, Ted
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Rameaka, Joshua G
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Price, Jennifer
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US-09-294-093B-2999; Sequence 2999, Ap
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; SEQ ID NO 2803
; LENGTH: 356
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-020-Q1-B1-B11
US-09-878-574-2803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules an
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2803, Application US/09878574 Patent No. US20020110548A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1999-06-14
                                                                                                                                                                                                                                1656 ACTAGTGCTTCCTGATGGATCGATCCTTCGAAGTGAGTACTATGCACTCCCGACTCGCGA 1715
                                                                                                                                                                                                                                                                                                   1596 TGGTGGCCCGATCTATGTTAGTGATTCTGTGGGAAAGCATAACTTTGATCTTCTGAAAAA 1655
                                                                                                                                                                                                                                                                                                                                                                                                     1536 GGATATGTTCCAATCCACCCACCCTTGTGCCGCCTTCCATGCTGCCTCTCGAGCCATCTC 1595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1476 TCACATGGTTCATTGTGCCAACGACAGCTTGTGGATGGGGGAACTTCATCCACCCTGACTG 1535
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                                                                                                          331
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                                                                                                                                               TTGTTTGTTTGAAGACCCT 1734
                                                                                                                                                                                                                                                                                                                                                                                                                                               TCACATTGCATCAGTGGCTTACAATACTATTTTCCTTGGTGAATTTATGCAGCCAGACTG 150
                                                                                                                                                                                           GCTTGCACTACCTGATGGTTCTATATTAAGGGCTAAACTTCCAGGACGACCAACAAAGGA
                                                                                                                                                                                                                                                                                                                                                              GGATATGTTTCATAACCTACATCCGATGGCTGAATATCATGGTGCAGCACGAGCTGTATG 210
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Application US/09294093B
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules a
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR APPLICATION NUMBER: 09/333,535
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                                                                                                                                                                      NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 1840
LENGTH: 377
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: LIB3028-032-Q1-B1-E5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1840, Application Patent No. US20020110548A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. US20010051335A1 GENERAL INFORMATION:
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SEQ ID NO 2999
                                                                                                             Query Match
                                                                           Matches
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Best Local Similarity
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CURRENT FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/082,567
PRIOR FILING DATE: April 21,1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ito, Laura, Y.
APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLYNICLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
FILE REFERENCE: PL-0009 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
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LOCATION: 190, 193-194, 206, 217, 232,
OTHER INFORMATION: a, t, c, g, or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature OTHER INFORMATION: Incyte ID No. US20010051335A1 700347006H1
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ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 296
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217
                                  192 TGGTTGCTTTGTTGGATTCGACGCGTCGGAACCTGATAGCCGACATGTTGTTTCGATTGG 251
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mes 89; Conserv
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TGGGGCATTCATTGGGGTTCAATCCCATCACAAGGGTAGCCGCACAGTCTTCCCAATTGG 276
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                                                                           Conservative
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April 21, 1998
                                                                                           1.9%;
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                                                                         Score 45.8; DB 10;
Pred. No. 0.00068;
0; Mismatches 72;
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Pred. No. 2.4e-13;
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                                                                                                           Length 377;
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RESULT 6
US-09-866-570A-19
Sequence 19, Application US/09866570A
Patent No. US20020168745A1
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: Transacylases of t
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; ORGANISM: Arabidopsis thaliana
US-09-770-696-410
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                                                                                                                                                                                                                                                                                                                                                                                          Query Match 1.9%;
Best Local Similarity 57.0%;
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CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,278
PRIOR FILING DATE: 2000-01-27
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                                                                                                                                                                                            1231 CACCTATTGGAGATGTTGTGTG 1252
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                                                                                                                                                                            131 TGTGTATTGGAGACTTTGGGTG 152
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Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
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Rameaka, Joshua G
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Hurban, Patrick
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Slader, Ted
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                             Transacylases of the Paclitaxel Biosynthetic Pathway
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Pred. No. 0.001;
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 911
; TYPE: DNA
; ORGANISM: Taxus cuspidata
US-09-866-570A-19
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SEQ ID NO 21
LENGTH: 911
TYPE: DNA
ORGANISM: Taxus cuspidata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION: APPLICANT: Croteau,
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Best Local
                                                                                                                                                                                                                                     Query Match
Best Local :
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                                                                                                                                                                                                                        Matches
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PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patantto ""
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CURRENT APPLICATION NUMBER: US/09/866,570A
CURRENT FILING DATE: 2001-05-25
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CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US/09/457,046B
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
                                                                                                                                               461
                                                                                                                                                                                317 TTGGTCGAAATGGTGGGGATCTTGAATCGGAGACTCAGATTGTGATCCTTGAGAAGTCAG 376
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TTCAAATTCCACATACTGAGAATGTGAAGCTTCTCTTTGCGATGGATTTGAGGAAATTAT
                                TTCAGCCTGGGGATGATGACTTTGTCGATGTTTGTCGAGAGTGGTTCGTCGAAAGTTG
                                                                      ATTTTTGTTCGTCCTTTGAAGTAGTGGCAGCATTGGTTTGGATAGCAAGGACAAAGGCTC
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Pred. No. 0
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; TYPE: DNA
; ORGANISM: Taxus cuspidata
US-09-866-572A-21
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Sequence 19, Application US/09866572A
Patent No. US20020138859A1
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
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; CRCANISM: Taxus cuspidata
US-09-866-572A-19
                                                                                                                                                                                                                                                                                                                                   US-09-866-572A-21
                                                                                                                                                                                                                                                                                                                                                         RESULT 9
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                                                      SEQ ID NO 21
LENGTH: 911
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
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Best Local Similarity
                                                                                                                                                                        APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic
FILE REFERENCE: 53679
CURRENT APPLICATION NUMBER: US/09/866,572A
CURRENT FILING DATE: 2001-05-25
                                                                                                           CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 09/457,046
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 74
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CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 09/457,046
PRIOR FILING DATE: 1999-12-07
                                                                                               SOFTWARE: PatentIn Ver. 2.1
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RESULT 11
US-10-091-504-1271
; Sequence 1271, Application US/10091504
; Publication No. US20030059908A1

GENERAL INFORMATION:

APPLICANT:

Rosen et al

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APPLICANT: MERKULOV, Gennady et al.
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL001196
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 3
                                                                                                                                                                                                                                   Query Match
Best Local :
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Best Local Similarity
Matches 116; Conserv
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                         30070 CCCAGGAGGCGGAGGTTGTGGTGAGTCGAGATCGCACCATTGCACTCCAGCCTGGGCAAC
                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature LOCATION: (1)...(46050
                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapien FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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TGCCAATAAATATGGAAAAAAAAAAAAGGCTCAACTT 30225
                    CTCTATTGAAGGCGTTAAAAACCTTTGCGCTTTACCT 1964
                                                                   ACGAGTGACATCCAAAACTAACCCAAAAGACATAGAATGGCACAGTGGAGAAAACCCTAT
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Pred. No.
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Pred. No. 7.7;
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hes 130; Indels
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Sequence 1272, Application US/10091504
Publication No. US20030059908A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PC007C1
CURRENT APPLICATION NUMBER: US/10/091,504
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 2442
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US-09-764-869-1271
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US-10-091-504-1272
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US-10-091-504-1272
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                                  GENERAL INFORMATION:
                                                     Sequence 1271, Application US/09764869 Patent No. US20020061521A1
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Best Local :
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Best Local
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CURRENT FILING DATE: 2002-03-07
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 APPLICANT: ROSEN et
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 2442
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Local Similarity 53.0%;
les 80; Conservative
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Nucleic Acids,
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Pred. No. 0.88; 
0; Mismatches 71;
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; SOFTWARE: PatentIn Ver. 2.0
; SEO ID NO 1271
; LENGTH: 1664
; TYPE: DNA
; ORGANISM: HOMO sapiens
US-09-764-869-1271
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; TYPE: DNA
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US-09-764-869-1272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1272, Application US/09764869 Patent No. US20020061521A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: PC007
CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
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1107
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                               1902 AGAATGGCACAGTGGAGAAAACCCTATCTCT 1932
                                                                                                     1842 CAACCAATGCTTTTCACAATACTCAAAACGAGTGACATCCAAAACTAACCCAAAAGACAT 1901
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Local Similarity 53.0%;
ses 80; Conservative
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AGAAAAAGAAAAGAAAACTTTTCCCT
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US-09-796-692-7801/c

Sequence 7801, Application US/09796692 Publication No. US20020198362A1 GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander APPLICANT: Algate, Paul A.

APPLICANT:

Mannion, Jane

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Вb
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Search completed: April Job time : 398 secs
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PRIOR APPLICATION NUMBER: 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR APPLICATION NUMBER: 60/206,201
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/218,950
PRIOR APPLICATION NUMBER: 60/223,903
PRIOR APPLICATION NUMBER: 60/223,416
PRIOR APPLICATION NUMBER: 60/223,416
PRIOR APPLICATION NUMBER: 60/223,416
PRIOR APPLICATION NUMBER: 60/223,416
PRIOR APPLICATION NUMBER: 60/223,378
PRIOR FILING DATE: 2000-08-07
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PRIOR FILING DATE: 2000-03-01
PRIOR PRIOR APPLICATION NUMBER: 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/200,084
PRIOR FILING DATE: 2000-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.6%; Score 37.2; DB 9; Length 441; Best Local Similarity 57.9%; Pred. No. 0.4; Matches 66; Conservative 0; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 9597
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7801
LENGTH: 441
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                                                                                                                                     1809 CCAAGGAGGATGGTGTGTGAGACACGCCGCAACCAATGCTTTTCACAATACTCAAA 1868
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Maximum DB
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Listing first 45 s
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Perfect score:
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     Issued_Patents_AA:*
1: /cgn2_6/ptodata/1.
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4: /cgn2_6/ptodata/1.
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 262574 seqs, 29422922 residues
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US-09-350-769-21
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US-09-164-922-2
US-09-874-562-7
US-09-890-115-16
US-09-491-362-7
US-09-494-335-6
US-09-449-335-6
US-09-480-921B-10
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sequence
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3, Appl
21, Appl
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AMAADAAAMDQDGA 	ch l Simi 14;	FAX: (7 FOR TION FOR ICE CHARA STH: 14 S: amino COLOGY: 1 COLOGY:	APPLICATION NUMBER: FILING DATE: FILING DATE: TOTORNEY AGENT INFORMAT NAME: NORMAN F. OBLO REGISTRATION NUMBER: REGISTRATION NUMBER: TELEPHONE: (703) 413	COUNTRY: UZIP: 22202 ZIP: 22202 DMPUTER READ MEDIUM TYPE COMPUTER: COMPETING S SOFTWARE: SOFTWARE:		OHENE ZZZ	ωω,	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
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PWP 14	/at	AX: (703)-413-2220 ON FOR SEQ ID NO: E CHARACTERISTICS: H: 14 amino acids amino acid GGY: linear GGY: linear T TYPE: peptide T TYPE: internal	UMBER: US/G INFORMATION: F. OBLON NUMBER: 24, ON INFORMATION 1NFORMATION 1NFOR	E FORM: Floppy PC com EM: PC entin F	a . 69 .	Ch Ch Tak	ion	138	744 747 758 758 758 758 758 758 758 758 758 75
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-846-234-5
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SOFTWARE: Pac
SEQ ID NO 21
SEQ TO NO 21
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SEQUENCE CHARACTERISTICS:
LENGTH: 784 amino-
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Patent No. 63233
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Best Local Similarity
                                                                                                                                       APPLICANT: METCALE, Donald
APPLICANT: METCALE, Donald
APPLICANT: NICOLA, NICOS A
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC AGENTS
FILE REFERENCE: 109762
                                                                         CURRENT APPLICATION NUMBER: US/09/302,769
CURRENT FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: 08/962,560
PRIOR FILING DATE: 1997-10-31
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                                                          NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/846,234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: OSUMI Chiek
APPLICANT: NOZAKI Jins
APPLICANT: KIDA Takao
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                                         SEQ ID NOS: 50 PatentIn Ver. 2.0
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NICHOLSON, Sandra E
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VINEY, Elizabeth M
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NOZAKI Jinshi
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Pred. No. 5.9e-06;
Pred. No. 5.9e-06;
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TRANSGENIC
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 527
TYPE: PRT
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Best Local :
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APPLICANT: TESTA, TANIA TANSON
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30218
CURRENT APPLICATION NUMBER: US/09/659,166
CURRENT FILING DATE: 2000-09-11
                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: William T. Han
REGISTRATION NUMBER: 34,
                                                             APPLICATION NUMBER: US/08/802
FILING DATE: 19 February 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOTTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                            ZIP: 19406
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 YDDDQGSYVQVP 140
                                                                                                                                                                                                                                                                                    ADDRESSEE: SmithKline
STREET: 709 Swedeland
CITY: King of Prussia
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                                                 FILING DATE
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BER: UK 9921505.5
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66.7%;
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Pred. No.
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                                                                                                             US-09-350-484-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09350484
Patent NO. 6159716
GENERAL INFORMATION:
APPLICANT: Creasy, et al.
TITLE OF INVENTION: HUMAN PROTEIN KINASE HOACE72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                    Query Match
Best Local :
                                   Matches
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                 TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 YDDDQGSYVQVP 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
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1 YDQDQMVVVQVP 12
                                                                                                                                           STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                    NAME: William T. Han
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/802,466 FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 19406
COMPUTER READABLE FORM:
                                                                                                                        MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                   Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/350,484 FILING DATE: 09-Jul-1999 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 709 Swederaum CITY: King of Prussia
                                                                                                                                                                                             TYPE: amino acids
                                                                                                                                                                                                                                                                                      TELEPHONE: 610-270-5219
TELEFAX: 610-270-4026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road
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                                     Conservative
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                                                  Score 38; DB
Pred. No. 79;
                                   Mismatches
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                                                                   4; Length 528;
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US-09-157-420-1
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; LENGTH: 1829
; TYPE: PRT
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Patent No. 6222095
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APPLICANT: NAKANISHI, Hiroyuki
APPLICANT: MANDAI, Kenji
APPLICANT: WADA, MANABU
APPLICANT: WADA, MANABU
APPLICANT: OBAISHI, Hiroshi
TITLE OF INVENTION: ACTIN FILAMENT-BINDING PROTEIN "L-AFADIN"
FILE REFERENCE: 98-1042*/LC(WMC)/653
CURRENT APPLICATION NUMBER: US/09/157,420
CURRENT FILING DATE: 1998-09-21
NUMBER OF SEQ ID NOS: 1
                                                                     TELEFAX: (415) 576-030 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,922
FILING DATE: 22-APR-1998
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Callis, Judy
APPLICANT: Worley, Cathy K.
TITLE OF INVENTION: Sequence
TITLE OF INVENTION: Product.
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1246 QDRMAPVQNQWP 1257
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Hyman, Laurence J.
REGISTRATION NUMBER: 35,551
REFERENCE/DOCKET NUMBER: 02
                              SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 YDDDQGSYVQVP 141
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STATE: California
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FOPOLOGY:
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7; Conserv
                amino acid
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Pred. No. 3.4e+02;
Pred. No. 3.4e+02;
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Length 1829; Indels

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for Degradation

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US-09-491-362-7
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Best Local Similarity
Thes 7; Conservat
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             Sequence 7, Application US/09491362
Patent No. 6281017
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney B
APPLICANT: Lange, Bernd M
TITLE OF INVENTION: 1-DEOXY-D-XYLULOSE-5-PHOSPHATE REDUCTOISOMERASE, AND
TITLE OF INVENTION: METHODS OF USE
FILE REPERENCE: WSUR14977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 58...
7; Conservative
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CURRENT APPLICATION NUMBER: US/09/491,362
                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 179 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Hyman, Laurence J.
REGISTRATION NUMBER: 35,551
REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09
FILING DATE: 22-APR-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Hyman, Laurence J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Callis, Judy
APPLICANT: Worley, Cathy K.
TITLE OF INVENTION: Sequence
TITLE OF INVENTION: products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                           135 DGDWMLVGDVPW 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 DGDWMLVGDVPW 123
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STATE: California
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                                                                                                                                                                                                                                                                                                                 46.2%; ilarity 58.3%; Conservative
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58.3%;
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                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                    Score 37; DB Pred. No. 33;
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Pred. No. 28;
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US-08-764-870-16
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Best Local Similarity
"~+~hes 6; Conserv?
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; TYPE: PRT
; ORGANIZM: Arabidopsis thaliana
US-09-491-362-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-874-562-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Croteau, Rodney B
APPLICANT: Lange, Bernd M
TITLE OF INVENTION: 1-DEOXY-D-XYLULOSE-5-PHOSPHATE REDUCTOISOMERASE,
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: WSUR17549
CURRENT APPLICATION UNMBER: US/09/874,562
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION UNMBER: 09/491,362
PRIOR APPLICATION UNMBER: 09/491,362
PRIOR APPLICATION UNMBER: 09/118,349
PRIOR PILING DATE: 1999-02-03
NUMBER OF SEQ ID NOS: 13
NUMBER OF SEQ ID NOS: 13
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EARLIER APPLICATION NUMBER: 60//
EARLIER FILING DATE: 1999-02-03
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                              Sequence 16, Application US/08764870 Patent No. 6236946
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                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 399
TYPE: PRT
                                                                                                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                   APPLICANT: Apriletti, James W
APPLICANT: West, Brian
TITLE OF INVENTION: Nuclear Receptor
TITLE OF INVENTION: Binding Domains
                                                                                                                                                                                 APPLICANT:
                                                                  CORRESPONDENCE ADDRESS:
                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                           254 QDSSVLAQLGWP 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254 QDSSVLAQLGWP 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.2%;
Local Similarity 50.0%;
nes 6; Conservation
                                  STREET:
                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                             3 QDQMVVVQVPWP 14
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Palo Alto
: CA
                                  E: Cooley Godward
Five Palo Alto Square,
                                                                                                                                                                               Fletterick, Robert J
Wagner, Richard L
Kushner, Peter J
                                                                                                                                                                                                                                       Baxter, John D
                                                                                                                                                                                                                                                        Scanlan,
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50.0%;
                                                                                                                                                                                                                                                          Thomas S
                                                                                                                          Nuclear Receptor Ligands and Ligand
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37;
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                                    3000 El Camino Real
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85;
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0;

Gaps

0;

COUNTRY:

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APPLICANT: WEST, Brian L.

APPLICANT: Shibu, Andrew K.

TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOMAINS
FILE REFERENCE: UCAL-246/02US
CURRENT APPLICATION NUMBER: US/08/980,115
CURRENT FILING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: 08/764,870
EARLIER FILING DATE: 1996-12-13
EARLIER FILING DATE: 1996-12-13
EARLIER FILING DATE: 1995-12-14
EARLIER FILING DATE: 1995-12-14
EARLIER APPLICATION NUMBER: 60/008,543
EARLIER APPLICATION NUMBER: 60/008,543
EARLIER APPLICATION NUMBER: 60/008,543
SARLIER APPLICATION NUMBER: 60/008,540
EARLIER APPLICATION NUMBER: 60/008,540
EARLIER FILING DATE: 1995-12-13
SOFTMARE: PATENT DATE: 1995-12-13
SOFTMARE: PATENT DATE: 1995-12-13
NUMBER OF SEO ID NOS: 17
SOFTMARE: PATENTIN Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16, Appl. Patent No. 626662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -08-980-115-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,540
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,543
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,606
APPLICATION NUMBER: US 60/008,606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wagner, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Apriletti, James W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (560)843-5000
NFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: UC
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/008,606
FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: NAKAMULTA, Jackie N
REGISTRATION NUMBER: 35,966
PROTESTINATION NUMBER: 35,966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265 DQMAVIQYSW 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 13-DEC CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 DOMVVVQVPW 13
                                                                                                                                                                                                                                                                                                                                                                                                                                        Kushner, Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baxter, John D.
Fletterick, Robert J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scanlan, Thomas S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08980115
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; NAME/KEY: DOMAIN
; LOCATION: (184)..(437)
; OTHER INFORMATION: minimal ligand binding domain
US-08-980-115-16
                                  ; ORGANISM: Mentha piperita US-09-874-562-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Mentha piperita US-09-491-362-2
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; Sequence 2, Applic

; Patent No. 6281017
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US-09-874-562-2
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Best Local S
Matches 6
                                                                                                NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Croteau, Rodney B
APPLICANT: Lange, Bernd M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENCTH: 475
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Croteau, Rodney B
APPLICANT: Lange, Bernd M
TITLE OF INVENTION: 1-DEOXY-D-XYLULOSE-5-PHOSPHATE REDUCTOISOMERASE,
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: WSUR14977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09874562 Patent No. 6420159
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/874,562
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 09/491,362
PRIOR FILING DATE: 2000-01-26
                                                                                                                                                                                                                                                        TITLE OF INVENTION: 1-DEOXY-D-XYLULOSE-5-PHOSPHATE REDUCTOISOMERASE, AND TITLE OF INVENTION: METHODS OF USE FILE REFERENCE: WSUR17549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: 60/118,349 EARLIER FILING DATE: 1999-02-03 NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2000-01-26
                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/118,349 PRIOR FILING DATE: 1999-02-03
                                                                  LENGTH: 475
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 331 QDSSVLAQLGWP 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity hes 6; Conserv
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nes 6; Conservative
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46.28;
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Score 37;
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Pred. No.
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DB 4;
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Length 475;
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Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 3 COMMYNOPPHP 14

Db 331 COSSYLAQLIGHP 342

Search completed: March 27, 2003, 10:07:35

Job time: 4.41463 secs
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Minimum DB
Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein - protein search, using sw model
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                                                                                                                                                                                               Score
                                                                                                                                                                                                                                                                                      re greater than is derived by a
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   4455555666
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length: 2000000000
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Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100
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Gapop 10.0 , Gapext 0.5
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80
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                                                                                                                                                                                                                                                                                                                                                    /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*
0. /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*
1. /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*
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5. /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*
7. /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:*
8. /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*
9. /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
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11. /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*
22. /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA20000.DAT:*
23. /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA20001.DAT:*
24. /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA20001.DAT:*
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Listing first 45 summaries
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
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AAW53569
AAY17424
AAW517417
AAB98659
AAW57887
AAW57887
AAW57887
AAW57840143
AAB93664
AAU67218
                                                                                                                                                                                                                                                  SUMMARIES
             Cucumber raffinose
Cucumber raffinose
Soybean protein: S
Soybean raffinose
Amino acid sequenc
Soybean raffinose
Herbicidally activ
                                                                                                                                                                                Description
                                                                                                                                           Cucumber raffinose
Cucumber raffinose
Propionibacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1
AAW53569
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Arabidopsis thalia	AAG53160	21	692	2	42	Ψ.
Human per	ABG43149	23	9	2	42	
Peptide #	AAM33498	22	90	Ņ	42	_
Peptide #63	AAM19912	22	90	N	42	
Human bone ma	AAM73298	22	90	Ņ	42	
Human brain ex	AAM60626	22	90	2	42	Ĭ
Peptide #7392 e	ABB39886	22	90	Ν	42	_
Chicken oocyte r	AAR78233	16	6	ω	43	_
Soybean rhgl	AAM42231	22	877	55.0	44	_
Soybean rhgl lee	AAM42229	22	7	ŗ	44	٠.
Soybean rhg1	AAM42227	22	7	5	44	٠.
Soybean rhgl	AAM42221	22	7	ū	44	
Soybean rhgl	AAM42219	22	7	ŗ	44	_
Soybean rhgl	AAM42232	22	ū	S	44	
Soybean rhgl	AAM4 2230	22	S	5	44	•
Soybean rhg1 nc	AAM42228	22	854	5	44	Ŭ
Soybean rhigh toy	AAM42222	22	G	5	44	_
Soybean rhg1 peki	AAM42220	22	G	ŗ.	44	_
Soy bean SCN/SC	ABB10122	22	830	5	44	_
Soybean raffinos	AAY70978	21	5	ŗ.	44	٠.
Arabidopsis thal	AAG52083	21	7	5	44	•
Arabidopsis thal	AAG52084	21	w	5	44	
Arabidopsis	AAG52085	21	w	5	44	_
Arabidopsis t	AAG07532	21	7	ū	44	
Arabidopsis thal	AAG45845	21	9	5	44	•
Arabidopsis t	AAG45846	21	N	5	44	_
Arabidopsis	AAG07533	21	N	5	44	_
Arabidopsis t	AAG45847	21	N	ŗ	44	_
Arabidopsis	AAG07534	21	N	5	44	
Mustard raffi	AAY32074	20	7	6.	45	-
Arabidopsis theli	AAG53155	21	8	٥.	45	-
Rapeseed raff	AAY32075	20	7		45	
Arabidopsis	AAG53156	21	9	5	45	
Arabidopsis	AAG53157	21	8	σ,	45	
Propionibacterium	AAU49825	22	4	7	46	

ALIGNMENTS

Cucumber raffinose synthase residues 756 to 769.

06-JUL-1998 (first entry)

AAW53569;

AAW53569 standard; peptide; 14

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The present sequence is a cucumber raffinose synthase fragment.
                                      Raffinose synthase gene - useful for preparation transformed plant % \left( 1\right) =\left\{ 1\right\} 
                                                                                                         26-JUL-1996;
26-APR-1996;
                                                                                                                                                         07-APR-1998
                                                                                                                                                                           JP10084973-A.
                                                                                                                                                                                               Cucumis sativus
                                                                                                                                                                                                                 Cucumber; raffinose synthase; sucrose; galactinol
                   Example 2; Page 17; 26pp;
                                                                   WPI; 1998-264858/24.
                                                                                                                                      28-APR-1997;
                                                                                     (AJIN ) AJINOMOTO KK
                                                                                                         96JP-0198079.
96JP-0107682.
                                                                                                                                      97JP-0111124
                   Japanese.
                                                 of.
                                                 raffinose in
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RESULT 3
AAW53570
ID AAW5
XX
AC AAW5
XX
DT 06-J
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AAY17424
                                                                                                                                                    밁
                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy
                                                                                                                                                                                                                  Query Match
Best Local S
Matches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                            The present invention describes a raffinose synthase, having an activity of forming raffinose from sucrose and galactinol. The raffinose synthase gene can be used for expression in a plant for the production of raffinose. The raffinose synthase can give raffinose from sucrose and galactinol efficiently. The present sequence represents a raffinose contraction of the contra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Raffinose synthase forms raffinose from sucrose and galactinol, has an optimum pH of 6 to 8 and working temperature of 35 to 40 degrees C, has a molecular weight of 75 to 95 kDa by gel filtration or 90 to 100 kDa by PAGE and SDS-PAGE under reductive conditions and is inhibited by iodoacetamide, N-ethylmaleimide and myoinositol.
   06-JUL-1998
                                   AAW53570;
                                                                AAW53570 standard;
                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                synthase peptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                               New raffinose synthase gene - sucrose and galactinol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JP11123080-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cucumis sativus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cucumber raffinose synthase peptide SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY17424 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-340516/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 22; 37pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AJIN ) AJINOMOTO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Raffinose synthase;
                                                                                                                                                    Local Similarity
                                                                                                                                                                                 1 YDQDQMVVVQVPWP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 YDQDQMVVVQVPWP
                                                                                                                                                  YDQDQMVVVQVPWP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YDQDQMVVVQVPWP
                                                                                                                                                                                                                   14;
                                                                                                                                                                                                                                                                                    14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 AA;
                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97JP-0292969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97JP-0292969
                                                                  Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14
                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sucrose;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                 cucumber.
                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               galactinol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 80; DB Pred. No. 1.7
D; Mismatches
                                                                                                                                                                                                                                 Score 80; DB 20;
Pred. No. 1.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for production of raffinose from
                                                                  A
                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 19;
1.7e-07;
thes 0;
                                                                                                                                                                                                                                                Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 14;
                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                  an activity
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                 synthase
                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
AAY17417
ID AAY1
   PR XX PA DR DR PT PT
                                                                                                                                                  XX PXX PXX OS XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X X C C C C C X X X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PT XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 14
sucrose and galactinol
                                               WPI; 1999-340516/29
N-PSDB; AAX61238.
                                                                                                                                                                                                                                                                 Cucumis sativus
                                                                                                                                                                                                                                                                                                                                 Cucumber raffinose
             New raffinose synthase gene -
                                                                                                                                 24-OCT-1997;
                                                                                                                                                                  24-OCT-1997;
                                                                                                                                                                                                  11-MAY-1999.
                                                                                                                                                                                                                                 JP11123080-A.
                                                                                                                                                                                                                                                                                                                                                                 29-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                  AAY17417;
                                                                                                                                                                                                                                                                                                                                                                                                                                AAY17417 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-264858/24.
N-PSDB; AAV22250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUL-1996;
26-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JP10084973-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cucumber;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cucumber raffinose synthase
                                                                                               (AJIN ) AJINOMOTO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transformed plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cucumis sativus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AJIN ) AJINOMOTO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               756 YDQDQMVVVQVPWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 YDQDQMVVVQVPWP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             784 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                 97JP-0292969
                                                                                                                                                                  97JP-0292969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96JP-0198079
96JP-0107682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97JP-0111124
                                                                                                                                                                                                                                                                                                                               synthase
                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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01.1 √4.2 ∰

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The present sequence is cucumber raffinose synthase, which forms raffinose from sucrose and galactinol, has an optimum pH of 6 to 8 and working temperature of 35 to 40 degrees C, has a molecular weight of 75 to 95 kDa by gel filtration or 90 to 100 kDa by PAGE and SDS-PAGE under reductive conditions and is inhibited by iodoacetamide, N-ethylmaleimide and myoinositol.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Raffinose synthase; sucrose; galactinol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Pages 17-20; 26pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Raffinose synthase gene - useful for preparation of raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 80; DB
Pred. No. 1.5
); Mismatches
  tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sucrose;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ΑA
production of raffinose from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             galactinol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 19;
1.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'n
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RESULT 5
AAB98659
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밁
                                            Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 14
                                                                                                                             The present invention relates to a mutant protein of raffinose synthase in which at least one aromatic amino acid present at the position of about 1-7 amino acids from the N-terminus is deleted or replaced. The mutant protein can be used for reducing the raffinose oligosaccharide content in a plant body. The present protein from soybean, was used in the present in a plant body.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of forming raffinose from sucrose and galactinol. The raffinose synthase gene can be used for expression in a plant for the production of raffinose. The raffinose synthase can give raffinose from sucrose and galactinol efficiently. The present sequence represents raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2;
                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                09-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                        JP2001078783-A
                                                                                                                                                                                                                                                                                                                                                                                                                             Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    \begin{tabular}{ll} \textbf{Mutant: mutein: raffinose synthase: raffinose oligosaccharide reduction: } \\ \textbf{plant: soybean.} \end{tabular}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB98659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB98659 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      synthase from cucumber.
                                                                                                                                                                                                                              Novel mutant protein of raffinose synthase is useful for raffinose oligosaccharide content in a plant body -
                                                                                                                                                                                                                                                                    WPI; 2001-313373/33.
N-PSDB; AAH27438.
                                                                                                                                                                                                                                                                                                                                                       03-JUL-2000; 2000JP-0200571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soybean protein: SEQ ID 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                               27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention
                                                                                                                                                                                                                                                                                                        (SUMO ) SUMITOMO CHEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YDQDQMVVVQVPWP 14
|||||||||||||
756 YDQDQMVVVQVPWP 769
757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100 es 14; Conservative
                     3 QDQMVVVQVPWP 14
                                                                                                                     present
EDKMLRVQVPWP 768
                                             8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 25-27; 37pp; Japanese.
                                                                                             780 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              784 AA;
                                                                                                                      invention.
                                                                                                                                                                                                        Page 18-20;
                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                                                                                                                                                                                                                                                                                                99JP-0196036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                         662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 describes a raffinose synthase, having an activity
                                                                                                                                                                                                                                                                                                        CO LTD
                                                                                                                                                                                                      30pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                             υ
                                                          Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 80;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ξ
                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                         80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; DB 20;
. 1.5e-05;
ches 0;
                                                          DB 22;
2.9;
                                                                    Length 780;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                           reducing
                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                             Gaps
                                             0;
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RESULT

10-AUG-1999

JP11215984-A.

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AAW57887
ID AAW5
AAY30143
ID AAY3
                                                                                                                                                                                                                                                                                                                                           SXCCCCCCCCCX TX TT TX RR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
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                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                              This sequence represents the soybean raffinose synthetase of the invention. The raffinose synthetase is capable of producing raffinose by combining a D-galactosyl group through an alpha (1-6) bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule. The DNA can be used to modify metabolism of a host organism by introducing into the host organism or its cell so that the content of the raffinose family oligosaccharides are useful as food additives with beneficial effects on the gastrointestinal flora.
                                                Glycine max.
                                                                                                                                                  AAY30143;
                                                                                                                                                                           AAY30143 standard;
                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 31-34; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid molecule encoding plant raffinose synthetase capable of producing raffinose, used as food additives with beneficial effects on gastrointestinal flora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-324670/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gastrointestinal flora; soybean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Soybean raffinose synthetase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW57887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW57887 standard; Protein; 781 AA
                                                                       Raffinose synthase;
                                                                                                Amino acid sequence of a raffinose synthase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAV40801.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP849359-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Raffinose synthetase; metabolism modification; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-SEP-1998
                                                                                                                          26-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SUMO ) SUMITOMO CHEM CO LTD
                                                                                                                                                                                                                                         758
                                                                                                                                                                                                                                                                                         Local Similarity les 8; Conserv
                                                                                                                                                                                                                                                               3 QDQMVVVQVPWP 14
                                                                                                                                                                                                                                         EDKMLRVQVPWP 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wantanabe
                                                                                                                                                                                                                                                                                                                                         781 AA;
                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96JP-0338673.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97EP-0122417
                                                                                                                                                                           Protein; 781 AA
                                                                       plant; sucrose;
                                                                                                                                                                                                                                                                                                    62.5%;
                                                                                                                                                                                                                                                                                                   Score 50;
Pred. No.
                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                   DB 19;
2.9;
                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                               Length 781;
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Best Local S
Matches 8
  Query Match
                                             The
the
                   Sequence
                                    properties
                                                                       Example 6; Page 24-27;
                                                                                                                      N-PSDB;
                                                                                                                               WPI; 2001-104537/12.
                                                                                                                                                                                    30-APR-1999;
01-SEP-1999;
                                                                                                                                                                                                                                                                                                                         07-MAR-2001
                                                                                                                                                                                                                                                                                                                                          AAB49400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a raffinose synthase protein. The sequence is isolated from plant material. The protein forms raffinose by complexing alpha(1 to 6)- D-galactosyl hydroxyl group of the 6C of D-glucose residue in sucrose molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 8; Page 25-27; 40pp; Japanese.
                                                                                                   New soybean plant promoters useful for
                                                                                                                                                                                                              27-APR-2000; 2000EP-0108962
                                                                                                                                                                                                                                02-NOV-2000
                                                                                                                                                                                                                                                  EP1048733-A2
                                                                                                                                                                                                                                                                                     Plant promoter; transgenic
                                                                                                                                                                                                                                                                                                      Soybean raffinose synthase
                                                                                                                                                                                                                                                                                                                                                           AAB49400 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                 (SUMO ) SUMITOMO CHEM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New raffinose synthase gene - is prepared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-NOV-1997;
18-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-DEC-1997;
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mes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                 3 QDQMVVVQVPWP 14
:|:|: |||||
                                            present invention provides novel plant promoters which can be used production of transgenic plants which express genes with desired
                                                                                            desired
                                                                                                                                                                                                                                                                                                                                                                                                        EDKMLRVQVPWP 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1999-511112/43.
DB; AAZ10002.
                                                                                                                                                Ή,
                                                                                                                      AAC89523.
                                                                                                                                                Watanabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              781 AA;
                   781
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                                                                                           properties
                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                    99JP-0124527.
99JP-0247211.
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96JP-0338673.
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                                                                                                                                                                                                                                                                                                                                                           Protein;
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60
  62.5%;
                                                                       36pp;
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                                                                                                                                                 0eda
                                                                                                                                                                                                                                                                                     plant;
                                                                                                                                                                                                                                                                                                                                                            781
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Pred.
                                                                                                                                                <u>~</u>
 Score
                                                                         English
                                                                                                                                                                                                                                                                                                                                                           AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                   desired property.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 No ;
 50;
                                                                                                generating transgenic plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
2.9;
 DВ
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22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a plant material
Length 781;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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ABB93664
ID ABBC
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AAU67218
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Best Local :
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                           The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant
Propionibacterium acnes immunogenic protein #28114
                          27-FEB-2002
                                                                          AAU67218 standard;
                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                 Claim 5; SEQ ID NO 2875; 261pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                          are useful
                                                                                                                                                                                                                                                                                                                                                                                                         organisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-269010/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tietjen K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB93664 standard; Protein;
                                                                                                                                                                                                                                                            useful as
                                                                                                                                                                                                                                                                                    sequences are selected.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-AUG-2001; 2001WO-EP09892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200210210-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Herbicidal; plant; agriculture;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Herbicidally active polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB93664;
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                                                                                                                                     760 EDSMVMVQVPW 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          758 EDKMLRVQVPWP 769
                                                                                                                                                                                                 Local Similarity
                                                                                                                                                             3 QDQMVVVQVPW 13
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                                                                                                                                                                                                                                                           herbicides
                                                                                                                                                                                                                                                                      are selected. The polypeptides or nucleic acids encoding them for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weidler
                                                                                                                                                                                                                                    783 AA;
                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
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                                                                          Protein;
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                                                                                                                                                                                                 61.3%;
72.7%;
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                                                                                                                                                                                                 Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 2.9;
3; Mismatches
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                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 herbicide
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                                                                                                                                                                                                 DB
4.4;
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                                                                                                                                       RESULT 11
                                                                                                                                                                                                                                                                                                                                                                            the treatment, prevention and diagnosis of medical conditions caused by

C P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

C P. acnes is also involved in infections of bone, joints and the central
nervous system, however it is particularly involved in the inflammatory

C lesions associated with acnes in a patient comprises contacting a

Sample with a binding agent that binds to the proteins of the invention

and determining the amount of bound protein in the sample. The

C polypeptides may be used as antigens in the production of antibodies

specific for P. acnes proteins. These antibodies can be used to

C downregulate expression and activity of P. acnes polypeptides and

C therefore treat P. acnes infections. The antibodies may also be used as

C diagnostic agents for determining P. acnes presence, for example, by

C enzyme linked immunosorbent assay (ELISA).

C specification, but was obtained in electronic format directly from WIPO

c at fet with a bind activity of patent of the printed
                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 7
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Propionibacterium acnes immunogenic protein #10721
                                    27-FEB-2002
                                                                    AAU49825;
                                                                                                      AAU49825 standard; Protein; 148
                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequences AAU39105-AAU68017 represent Propionibacterium acnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; SEQ ID No 28413; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L'maisonneuve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-APR-2000; 2000US-199047P
02-JUN-2000; 2000US-208841P
07-JUL-2000; 2000US-216747P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-APR-2001; 2001WO-US12865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptides. The proteins and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                              Local Similarity
nes 7; Conserv
                                                                                                                                                                                           9 MTVVQIPWP 17
                                                                                                                                                                                                                            6 MVVVQVPWP 14
                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                 98
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                                                                                                                                                                                                                                                              Conservative
                                  (first entry)
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                                                                                                                                                                                                                                                                             57.5%;
77.8%;
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, Jen S, Carter
                                                                                                                                                                                                                                                            ; Score 46; DB 2; Pred. No. 1.5; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               their associated DNA sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pustulosis; hypertosis; osteomyelitis;
joint; central nervous system; ELISA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang
                                                                                                                                                                                                                                                                                               22;
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                                                                                                                                                                                                                                                                                             Length 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bhatia
                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunogenic
are used in
                                                                                                                                                                                                                                                              Gaps
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0

В

DX Z

18-OCT-2000

(first entry)

Arabidopsis thaliana protein fragment SEQ ID NO: 67650

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RESULT 12
AAG53157
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02-JUN-2000;
07-JUL-2000;
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AAG53157 standard; Protein; 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L'maisonneuve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
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                                                                                                                                                                                             9 MTVVQIPWP 17
                                                                                                                                                                                                                                                                         6 MVVVQVPWP 14
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                                                                                                                                                                                                                                                                                                                                                  Similarity 7; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-199047P.
2000US-208841P.
2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
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                                                                                                                                                                                                                                                                                                                                                                                  57.5%;
77.8%;
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, Jen S, Carter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                      Score 46; I
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                  Mismatches
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2.3;
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	signal transduction etic mapping; gene e
	pathway; m
	netabolic path
	<pre>pathway; promoter;</pre>
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JUN-199 JUL-199 JUL-19	3-JUN-199 3-JUN-199 4-JUN-199
99US-014082 99US-014128 99US-014128 99US-014128 99US-01428 99US-01428 99US-01428 99US-01428 99US-014362 99US-014400 99US-0144362 99US-014433 99US-014433 99US-014433 99US-014433 99US-014483 99US-014508 99US-014508 99US-014638 99US-014638 99US-014720 99US-014721 99US-014838 99US-014720 99US-014838 99US-014720 99US-014838 99US-014720 99US-014838 99US-014720 99US-014838 99US-014720 99US-014838 99US-014730 99US-014730 99US-014749 99US-014972; 99US-015068	-014

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RESULT 13
AAG53156
ID AAG53
XX AAG53
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KW Prote
KW hybri
KW termi
XX X
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Best Local S
Matches 7
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07-SEP-1999
17-SEP-1999
18-SEP-1999
16-SEP-1999
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29-SEP-1999
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13-OCT-1999
                                      Protein identification; signal transduction pathway; metabolic pathway; hybridiaation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                   AAG53156 standard;
           Arabidopsis thaliana
                                                                      Arabidopsis
                                                                                          18-OCT-2000
                                                                                                               AAG53156;
                                termination
                                                                                                                                                                                     457
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                                                                                                                                                                                     DEDEMLYGDDPWP 469
                                                                                                                                                                                                DQDQMVVVQVPWP 14
                                                                                                                                                                                                                            Similarity 53.17; Conservative
                              sequence
                                                                      thaliana protein fragment SEQ
                                                                                          (first
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99US-0153070.
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99US-01610080.
99US-0161105.
                                                                                                                                   Protein; 563
                                                                                          entry)
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Pred. No. 13;
3; Mismatches
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                                                                       NO:
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                                                                       67649.
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99US-0121825
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99US-0132487
99US-0134218
99US-0134218
99US-0134219
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RESULT 14
AAY32075
ID AAY32
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Best Local S
Matches 7
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22-SEP 1999
23-SEP 1999
24-SEP 1999
28-SEP 1999
29-SEP 1999
06-OCT 1999
06-OCT 1999
13-OCT 1999
11-OCT 1999
                         /note=
Misc-difference 143
        Misc-difference
                                                Misc-difference
                                                                    Misc-difference
                                                                                                    Brassica
                                                                                                                     Raffinose synthase; rapeseed;
                                                                                                                                          Rapeseed
                                                                                                                                                               17-JAN-2000
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                                                                                                                                                                                                                                                        536
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                                                                                                                                                                                                                                                        DEDEMLVGDDPWP
                                                                                                                                                                                                                                                                          DQDQMVVVQVPWP
                                                                                                                                                                                                                                                                                               h 56.2%;
Similarity 53.8%;
7; Conservative
                                                                                                   napus
                                                                                                                                          raffinose
                                                                                                                                                                                                       standard;
                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                       990S-015479
990S-0155139
990S-0155586
990S-0155658
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990S-0158029
990S-0158029
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990S-0159331
990S-0159584
990S-0169741
990S-0160741
990S-0160768
990S-0160768
990S-0160815
990S-0160815
990S-0160815
990S-0161406
                                              /note=
132
                                                                    Location/Qualifiers
        /note= "encoded by 144
/note=
                                                                                                                                          synthase
                                                                                                                                                                                                                                                                             14
                                                                                                                                                                                                       Protein; 572 AA
"encoded by
                                                        "encoded by
                                       "encoded
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Pred. No. 15;
3; Mismatches
                                                                                                                       transgenic
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TCR'
                    ccs"
                                                           GGY"
                                        GGW"
                                                                                                                                                                                                                                                                                                                    Length 563;
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01-JUL-1999
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99US-0144085.
99US-0144085.
99US-0144325.
99US-0144333.
99US-0145086.
99US-014720.

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RESULT 15
AAG53155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents rapessed raffinose synthase, a protein that can bind a D-galactosyl group through an alpha(1-6) bond to the hydroxy group attached to the carbon atom at the 6-position of the D-glucose residue in a sucrose molecule to form raffinose. cDNA (see AAZ20210) encoding the enzyme was isolated from rapessed cv. Westar leaf cDNA by PCR. Probes or primers generated from plant raffinose synthase genes (see AAZ20207-10) may be used to obtain other raffinose synthase genes by labeled detection or amplification (claimed). These genes may be used to control the levels of raffinose produced in plants. Antisense genes can be used to knock out existing gene activity, and sense genes to increase the level of gene activity. The resulting transgenic plants may be used as a food source to alter the growing conditions for gut enterobacteria, corroviding general health advantages.
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 199
N-PSDB;
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30-APR-1998;
04-DEC-1998;
 25-FEB-2000; 2000EP-0301439
                                06-SEP-2000
                                                        EP1033405-A2.
                                                                                    Arabidopsis thaliana.
                                                                                                              termination sequence.
                                                                                                                            Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control;
                                                                                                                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 67648
                                                                                                                                                                                                                                                      AAG53155 standard; Protein; 586 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New sense and antisense genes, useful for altering the level raffinose in food plants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Watanabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SUMO ) SUMITOMO CHEM CO LTD
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549 EESMVMVQVPW 559
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DB; AAZ20210.
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                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                           572 AA;
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                (first entry)
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98JP-0120551.
98JP-0345590.
98JP-0351246.
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                                                                                                                                                                                                                                                                                                                                                                                                 56.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                              20;
                                                                                                                                                                                                                                                                                                                                                                                                             Length 572;
                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                            pathway;
promoter;
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30-APR-1999
00-MAY 1999
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11-MAY 1999
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05-MAR-1999
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21-APR-1999;
23-APR-1999;
23-APR-1999;
28-APR-1999;
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16-APR-1999
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99US-0139463.
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990S-0134256

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                                                          559
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                                                         DEDEMLVGDDPWP
                                                                                                                  Similarity 53.7; Conservative
                                                                                                                                                                         990S-0156596

990S-0157753

990S-0157865

990S-0158369

990S-0158294

990S-0159294

990S-0159294

990S-0159330

990S-0159330

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990S-0161361

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990S-0161920

990S-0161920
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                                                                                    14
                                                          571
                                                                                                                                 56.2%;
               2003, 10:03:
                                                                                                                Score 45; DB Pred. No. 16; 3; Mismatches
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                                                                                                                                              Length
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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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      insecticyanin A -
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phosphonate metabo
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probable IAA6 prot
hypothetical prote
PTS system, IIC co
phosphotransferase
acetate-CoA ligase
probable phosphodi
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auxin-induced prot
hypothetical prote
IAA7 like protein
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androgen receptor
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RESULT 2 H71407 auxin-induced protein - C;Species: Arabidopsis t A;Variety: columbia C;Date: 03-Aug-1998 #seq C;Accession: H71407 R;Bevan, M: Bancroft, I P; Wedler, H.; Wedler, avanagh, T; Hempel, S; Nature 391 485-488, 199 A;Authors: Mueller-Auer, C; Chalwatzis, N. A;Title: Analysis of 1.9 A;Reference number: A714 A;Accession: H71407	Query Matc Best Local Matches Qy 2 DQ Db 120 DG	A; Accession: S58501 A; Status: nucleic a A; Molecule type: mR A; Residues: 1-164 < R; Theologis, A. submitted to the EM A; Reference number: A; Accession: S71408 A; Molecule type: DN A; Residues: 1-109; A; Cross-references: C; Genetics: A; Gene: IAA14 C; Superfamily: auxi	RESULT 1 S58501 auxin induced protein N; Alternate names: i. C; Species: Arabidops C; Date: 22-Nov-196 C; Accession: S58501; R; Abel, S: Nguyen, I J, Mol. Biol. 251, 5 A; Title: The PS-IAA4, A; Reference number: i	44444000000000000000000000000000000000
duced protein s: Arabidopsi s: Arabidopsi y: columbia 03-Aug-1998 # idon: H7107 M.; Bancroft ller, H.; Wedl T.; Hempel, 191, 485-488 s: Mueller Au A.; Moores, T watzis, N. Analysis of nnce number: A	2; D 000 -	ion: S58501 : nucleic aci le type: mRN/ es: 1-164 <ar \$="" \$71408="" 's'="" 1-109,="" a.="" amily:="" auxin-<="" cs:="" d="" dna="" e="" embi="" es:="" gis,="" iaa14="" ion:="" le="" nce="" number:="" references:="" td="" the="" to="" type:=""><td>duced prote ate names: s: Arabidop 22-Nov-1996 ion: S58501 s.; Nguyen, Biol. 251, The PS-IAA</td><td></td></ar>	duced prote ate names: s: Arabidop 22-Nov-1996 ion: S58501 s.; Nguyen, Biol. 251, The PS-IAA	
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Arab hali uenc .; B E.; Kot 8 S.; Jone	55. imilarity 61. ; Conservative ; Conservative HVVVQVPWP 14  :        :	cid sequence NA NBES BL Data Libr S71406 S71406 S',111-164 < EMBL:U18416	in IAA14 - Ar indoleacetic indoleacetic #sequence_re; \$71408 M.D.; Theolo \$33-549, 1995; 4/3-1ike fami	162 190 190 190 390 390 432 473 569 624 722 1206 1663 1663
bidopiana ce_re Bent, ; Wam tter, ; Sil es, J	0 . O . T		- Ar tic ana e_re e_re 1995	2222222222222222
th use ion ith tt, L; L; L; CG.; A 121	Score 44; Pred. No. 1; Mismat	ce not shown brary, December <the> 16; NID:9972930; protein aux28</the>	ALIGNMENTS  4 - Arabidopsis thallana toetic acid-inducible prolliana (mouse-ear cress) ance_revision 22-Nov-1996  B Theologis, A. Theologis, A	C82765 C64950 A90952 A90955 A70656 A70656 A70656 A706594 B96594 B96594 T30095 T42092 T30044 T30175
cress) Cress) Aug-1998 K.; Good Weitzeneg n, K.D.; ames, R.; va, T.; P va, T.; P sequence PMID:946	; DB 2; 1. 2; tches 4	oer 1994 930; PIDN:AAC49055.1;	TS laliana le prot ress) v-1996 v-1996 MID: 76:	
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lange Dea Poh M.; M.; Be	gth 164; Indels	<b>.</b>	vent) AA14 _change 2	conserved hypo yecm protein - hypothetical p hypothetical p pectinesterase hypothetical p glutamate-ammo probable beta- conserved hypo probable membu hypothetical p probable rever s-afadin - rate phosphodiester exoribonucleas
20-Jun-20 n, C.; Ber l, T.M.; T Schaeffer, Schaeffer, N.; Pons, A nes, V.; R	0;	PID:g972931	20-Aug-	conserved hypothetical hypothetical hypothetical pectinesteral splutamate amprobable bettonserved hypothetical probable mem hypothetical hypothetical hypothetical hypothetical hypothetical probable reversafadin rephasphodiest expression of the probable of the probable reversafadin.
20-Jun-2000 , C.; Bergkamp, T.M.; Terryn, chaeffer, M.; F ; Pons, A.; Put es, V.; Rechman mme 4 of Arabido	Gaps	772931	ıg-1999 Arabidopsis	conserved hypothet yecm protein - Esc hypothetical prote pectinesterase (EC hypothetical prote glutamate-ammonia probable beta-1,3-conserved hypothetical prote hypothetical protein hypothetical hypothetica
<b>д э - на</b>	0.		) lopsis	, se
mp, R.; D yn, N.; G ; Funk, B Puigdomen man, S.;			thal	
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IAA7 like protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 24-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C:Accession: .H86173

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alons R:Theologis, A.; Ecker, J.R.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, F. Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, F. Rature 408, 816-820, 2000

Rature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzial Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Southwick, A.M.; Sun, H.; Tallor A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallor A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A; Accession: H86173
                                           A; Map position: 4
C; Superfamily: au
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C; Superfamily: auxin-induced protein aux28
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A;Molecule type: DNA
A;Residus: 1-225 <BEV>
A;Cross-references: GB:Z97336; NID:g2244788; PIDN:CAB10234.1; PID:g2244811
                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-234 <STO>
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                                                                                    A; Gene: dl3315c
                                                                                                                           A;Cross-references: GB:NC_001268; NID:g5302771; PIDN:CAB46059.1; GSPDB:GN00140
                                                                                                                                                                                       A; Status: preliminary
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A; Residues: 1-229 <STO>
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les 8; Conserv
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                                         auxin-induced protein aux28
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Score 44;
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Pred. No.
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A; Note: F18021.
C; Superfamily:
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A; Accession: T47727
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein F18021.60 - Arabidopsis thaliana (;Speciles: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000 C;Accession: T47727
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T47727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: A86141; MUID:21016719; PMID:11130712
A; Reseasion: C86467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alo Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzin Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Talli ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                 A; Map position: 3
A; Introns: 244/2; 491/1; 511/1
                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-719 <BEN>
                                                                                                                                                                                                                                                                                                                                                                                                         R;Benes, V.; Wurmbach, E.; Drzonek, H.; Anssubmitted to the Protein Sequence Database,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE005172;
C;Genetics:
A;Map position: 1
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A;Molecule type: DNA
A;Residues: 1-619 <STO>
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                                                                                                                                                                                                                                                                                     A; Cross-references: EMBL: ATF18021
                                                                                                  Best
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Matches 8; Conservative
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                                                                                                                                                           unassigned Ser/Thr
                                                                               Conservative
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C:ACCESSION: AZZ--
R:GBO, Y:, Schofield, O.M.; Leustek, T.
Plant Physiol. 123, 1087-1096, 2000
A:Title: Characterization of sulfate assimilation
A:Title: Characterization of sulfate assimilation
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C; Access
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A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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C;Superfamily: Rickettsia prowazekii hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrol A;Reference number: A97359; PMID:11743194
A;Accession: G97360
                                                                                                                   5'-adenylylsulfate reductase (EC 1.8.99.-) [validated] - green alga (Enteromorpha C;Species: Enteromorpha intestinalis (hollow green seaweed) C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
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A;Residues: 1-418 <KUR>
A;Residues: 1-418 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL41046.1; PID:g17738332; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: The Genome of the Natural Genetic A; Reference number: AB2577; PMID:11743193 A; Accession: AH2578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-418 < KUR>
                                                                                                   C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE007869;
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7; Conser
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Rickettsia prowazekii hypothetical protein RP681
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87.5%;
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Pred. No. 8.8;
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                PMID:10889258
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8.8;
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                                  algae focusing
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F;45-863/Product: VLDL receptor status predicted <AMATY
F;45-787/Domain: EDL receptor ligand-binding repeat homology <LDL1>
F;90-126/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;90-126/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;131-167/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F;121-247/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F;211-247/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F;217-291/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F;26-330/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F;36-373/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F;378-412/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F;378-412/Domain: EDF homology <EG1>
F;499-549/Domain: EDF homology <EG2>
F;499-549/Domain: LDL receptor YWTD-containing repeat homology <YW3>
F;499-544/Domain: LDL receptor YWTD-containing repeat homology <YW3>
F;585-587/Domain: LDL receptor YWTD-containing repeat homology <YW3>
F;632-674/Domain: LDL receptor YWTD-containing repeat homology <YW3>
F;675-717/Domain: LDL receptor YWTD-containing repeat homology <YW6>
F;775-7760/Nomain: LDL receptor YWTD-containing repeat homology <YW6>
F;7767-7760/Nomain: LDL receptor YWTD-containing repeat homology <YW6>
F;7767-7760/Nomain: LDL receptor YWTD-containing repeat homology <YW6>
F;7760/Nomain: LDL receptor YWTD-containing repeat homology <YW6>
F;776
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F;169,773/Binding
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A; Residues: 1-863 <BUJ>
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C;Date: 14-Aug-1998 #sequence_revision
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A; Residues: 1-423 <GAO>
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A; Status: pre
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609
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nes 7; Conserv
                                                                                                                                                                             Local
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                                                                 YDQDQMVVVQVPWP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary;
FDRQQLVTTEIQWP
                                                                                                                                       Similarity 5; Conserv
                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                     transmembrane #status predicted <TMM>
coated-pit mediated internalization signal
site: carbohydrate (Asn) (covalent) #status predicted
site: carbohydrate (Asn) (covalent) #status predicted
,400-412,418-428,424-437,439-452,726-739,735-754,756-769/Disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                        EGF homology <EG3>
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                                                                                                                                                                         53.8%;
                                                                                                                                                                         Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 43; I
Pred. No. 8
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                                                                                                                                                                     DB 20;
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                                                                                                                                                                                                            Length 863;
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C;Genetics:
A;Gene: 40
C;Superfamily: varicella-zoster virus gene 38 protein
C;Superfamily: varicella-zoster virus gene 38 protein
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C;Accession: D86274
R;Theologis; A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Chin, C.W.; Chung, M.K.; Luiz, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C. A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, R.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Yitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                         R;Theologis, A.; Ecker, J.R.; Palm, Chin, C.W.; Chung, M.K.; Conn, L.; ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000
                                                                                                                                                         probable auxin response factor, 53188-50111 [imported] - Arabidopsis thalia
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tegument protein 40 - equine herpesvirus 4 (strain NS80567)
C;Species: equine herpesvirus 4
A;Variety: strain NS80567
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C;Accession: T42584
R;Telford, E.A.; Watson, M.S.; Perry, J.; Cullinane, A.A.; Davison, A.J.
                                                                                                                                                                                                                                                      C86468
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                                                                                                                                     C; Accession: C86468
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A; Residues: 1-529 <TEL>
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A; Residues: 1-500 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
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Best Local Similarity
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Best Local
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                                                                                                                                                                                                                                                                                                                                                               283 DEIILVEEPWP 293
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nes 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .; Watson, M.S.; Perry, J.; Cullinane, A.A.; Davison, 79, 1197-1203, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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50.0%;
  Jenkins,
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45.5%;
  J.;
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Pred. No.
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Pred. No.
                                                                         C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alo
Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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Johnson-Hopson,
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. 16;
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c.;
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                                                                                                                                                                                                                    Arabidopsis thaliana
Khan,
s.;
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Khaykin,
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  Kin,
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war, K.,
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A; Molecule type: DNA
A; Residues: 1-530 <TEL>
A; Cross-references: GB: M86664; NID: g330791;
                                                                                                                     C:Accession: F36799
R:Telford, E.A.R.; Watson, M.S.; submitted to GenBank, March 1992
A:Description: The DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; Wh Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, ansen, N.F.; Hughes, B.; Huizar, L.

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mait Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; S Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                         A; Reference number: A36805
A; Accession: F36799
                                                                                                                                                                                                                gene 40 protein - equine herpesvirus 1 (strain Ab4p)
C;Species: equine herpesvirus 1
A;Note: host Equus caballus (domestic horse)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #
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A;Gene: F1504.37
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics:
A;Map position: 1
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A; Residues: 1-767 <STO>
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A; Residues: 1-600 <STO>
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Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                621 EEDKMLVGEDPWP
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nes 6; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                             633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52.5%;
46.2%;
                                                                                                                     of equine
                                                                                                                                                                      McBride, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42; DB Pred. No. 26; 5; Mismatches
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                                                                                                                     herpesvirus-1
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    PIDN:AAB02476.1; PID:g330833
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Maiti, R.
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Nitelford, E.A.R.; Watson, M.S.; McDride, K.; Davison, A.J.

(Vicology 189, 304-316, 1992

A.Thile: The DAN sequence of equine herpesyvirus-1.

(NiBeferonce number: A41831; MNID:93295566; PMID:1318606

A.;Ontents: anototation; possible protein-cooling frames

A;Sote: neither amino acid nor nucleotide sequence is given

A;Sene: 40

C;Senetics:

Ouery Match

S1.29; Score 41; DB 1; Length 530;

Best Docal Similarity 36-48; Pred; Mo. 26;

Matches 4; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

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Search completed; March 27, 2003, 10:06:52

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     GenCore version 5.1.4_p5_4578 (c) 1993 - 2003 Compugen Ltd.
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P98165 gallus g
Q9x178 arabidop
P28972 equine h
Q38824 arabidop
Q55404 synechoc
P16688 escheric
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P20043 lactobacill	P10275 homo sapien	097775 pan troglod	Q9tt90 canis famil	P15207 rattus norv	P19091 mus musculu	097960 papio hamad	097952 macaca fasc	097776 eulemur ful	P35953 oryctolagus	P49699 oryctolagus	Q14451 homo sapien

ALIGNMENTS

## RESULT 1 AXIH_ARATH RC STRIN-CV. Columbia; RX MEDLINE-20105719; PubMed-11130712; RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S., RA Theologis A., Ecker J.R., Palm C.J., Ecker S.C., Brooks S.Y., RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y., RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y., RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y., RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W., RA Chung M.K., Conn L., Conway A.B., Creasy T.H., Dewar K., RA Chung M.K., Conn L., Conway A.B., Croway A.R., Creasy T.H., Dewar K., RA Chung M.K., Conn L., Reng J.-D., Fong B., Fujii C.Y., RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L., RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E., RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Liam B., RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Liam B., RA Langin-Hooper S., Liu Z.A., Luros J.S., Maiti R., Marziali A., Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A., RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A., RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I., RA Allanda M., Nguyen M., Nierman W.C., Osborne B.I., RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D., RA Sakano H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D., RA Sakano H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D., RA Wuterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M., RA Wuterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M., RA Wuterback T., Van Aken S., Venter J.C., Davis R.W., The College T. C., Miranda M., Van Danis R.W., The College T. C., Miranda M., Van Danis R.W., The College T. C., Liu S.Y., Venter J.C., Davis R.W., The College T. C., Liu S.Y., Venter J.C., Davis R.W., The College T. C., Liu S.Y., Venter J.C., Davis R.W., The College T. C., Liu S.Y., Venter J.C., Davis R.W., The College T. C., Liu S.Y., Venter J.C., Dav P93830; 049162; 16-OCT-2001 (Rel. 4 16-OCT-2001 (Rel. 4 15-JUN-2002 (Rel. 4 STRAIN-cv. Columbia; MEDLINE-98004476; PubMed-9342315; MEDLINE-98004476; Theologis A.; Rouse D., Mackay P., Stirnberg P., Estelle M., Leyser O.; "Changes in auxin response from mutations in an AUX/IAA gene."; Science 279:1371-1373(1998). Arabidopsis thaliana (Mouse-ear cress). Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis. SEQUENCE FROM N.A STRAIN=cv. Columbia; MEDLINE=98146427; PubMed=9478901; SEQUENCE FROM N.A., MUTANTS AXR3-1 AND AXR3-3, AND MUTAGENESIS LEU-16; ASP-118 AND PRO-121. (Auxin response 3). IAA17 OR AXR3 OR AT1G04250 OR F19P19.31. Auxin-responsive Nature 408:816-820(2000). "Protein-protein interactions among the Aux/IAA proteins."; Proc. Natl. Acad. Sci. U.S.A. 94:11786-11791(1997). SEQUENCE FROM N.A. AXIH_ARATH STANDARD; e protein IAA17 (Indoleacetic acid-induced 3). 40, Last sequence update) Last annotation update) PRT; AA. protein

SEQUENCE FROM N.A. STRAIN-CV. Columbia;

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01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Very low-density lipoprotein receptor precursor
                                                                       P98165;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
"RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced |
SSP consortium (Salk/Stanford/PEGC).";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: COULD ACT AS REGULATOR OF GENES RESPONSIBLE FOR
MEDIATING THE VARIOUS AUXIN-INDUCED EVENTS RESPONSIBLE FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Theologis A.; "Full Length cDNA of gene F19P19.31 (GI:4389514)."; submitted (JAN-2001) to the EMBL/GenBank/DDBJ datab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Goldsmith A.D., Lee J.M., Toriumi M.J., Yu G., Brook Chen H., Karlin-Neumann G., Kim C.J., Lam B., Miran P. Palm C.J., Shinn P., Southwick A.M., Davis R.W., Ecl
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Shinozaki K., Davis R.W.,
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L; AF040631; AAC39439.1; -...
AF040632; AAC39440.1; -...
L; AC000104; AAB70451.2; -...
L; AF336916; AAC53997.1; -...
L; AY070094; AAL49831.1; -...
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INDUCTION: BY AUXIN.

MISCELLANEOUS: Increased auxin response of mutants axr3-1 and miscellaneous: form an increased stability of AXR3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    axr3-3 may result form an increased stabil SIMILARITY: BELONGS TO THE AUX/IAA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           factors ARF1 and IAA24.
SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GROWTH (BY SIMILARITY).
SUBUNIT: Homo and heterodimers.
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                                                                                                                                                                                    DQDQMVVVQVPWP
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: SUPPRESSES THE AXR3-1 PHENOTYPE:
ASSOCIATED WITH L-88.
                                                                                                                                                                                                                                                                                                                              : SUPPRESSES THE AXR3-1 PHENOTYPE, ASSOCIATED WITH L-88.
: SUPPRESSES THE AXR3-1 PHENOTYPE;
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oks S.Y., Chao
nda M., Nguyen
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SMART; SM00179; EGF_CA; 2.
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SMART; SM000192; LDLa; 8.
SMART; SM00135; LY; 5.
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                                                           SIGNAL
                                                                                Endocytosis;
                                                                                              Glycoprotein; VLDL;
                                                                                                                                                                                                                                        Pfam; PF00057; ldl_recept_a; Pfam; PF00058; ldl_recept_b;
                                                                                                                                                                                                                                                                                                                          EMBL; X80207; CAA56505.1; HSSP; P01130; 1AJJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barber D.L., Sanders E.J., Aebersold R., Schneider W.J., "The receptor for yolk lipoprotein deposition in the chi J. Biol. Chem. 266:18761-18770(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Chicken oocyte growth is mediated by an eight ligand binding repeat member of the LDL receptor family."; EMBO J. 13:5165-5175(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=White leghorn; TISSUE=Ovary; MEDLINE=95045409; PubMed=7957081; Bujo H., Hermann M., Kaderli M.O., Nimpf J., Yamamoto T., Schneider W.
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Gallus gallus (Chicken).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                               InterPro; IPR002172; LDL_recept_A.
InterPro; IPR000033; Ldl_receptor_rep.
                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute.
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                                                                               Coated pits;
                                                                                                       ASX_HYDROXYL; 2.; ASX_HYDROXYL; 2.; EGF_1; FALSE_NEG.; EGF_2; 3.; EGF_CA; 2.; LDLRA_1; 8.; LDLRA_2; 8.
                                                                      Repeat.
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                                                                                              Cholesterol metabolism; Lipid
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LDL-RECEPTOR CLASS A 1.
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White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

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RA Chung P., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

RA Langin-Hooper S., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

RA Militscher J., Miranda M., Nugven M., Nierman W.C., Osborne B.I.,

RA Militscher J., Miranda M., Nugven M., Nierman W.C., Osborne B.I.,

RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,

"Sequence and analysis of chromosome 1 of the plant Arabidopsis
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Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Ke White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin
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Transferase; Glycosyltransferase; Golgi stack; C
SEQUENCE 500 AA; 57538 MW; 1C5BB6152BFAE690
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Sarria R., Wagner
Keegstra K., Raik!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                            STANDARD;
      24,
                                                                                                                                                                                                                                                                                                                                                                                                                             52.5%;
                                                                  Created)
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                                                                                                                                                                                                                                                                                                                                                                                                    Score 42; DB Pred. No. 6; 4; Mismatches
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Matches 4
Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S., White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y., Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W., Chung M.K., Conn L., Conway A.B., Conway A.B., Creasy T.H., Dewar K., Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y., Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y., Bill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L., Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E., Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B., Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P., Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Abel S., Nguyen M.D., Theologis A.; "The PS-IAA4/5-like family of early Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=cv. Columbia;
MEDLINE=95387393; PubMed=7658471;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Telford E.A.R., Watson M.S., McBride K., Davison "The DNA sequence of equine herpesvirus-1."; Virology 189:304-316(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=cv. Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no rest
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21016719; PubMed=11130712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92295566; PubMed=1318606;
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Pfam; PF03252; UL21; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 284
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MBL outstation -
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Palm C.J., Shi
Theologis A.;
                                                 Sugiura M., Tabata S.;
Sequence analysis of the genome of
Synechocystis sp. strain PCC6803. I.
                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Acetyl-coenzyme A synthetase (EC 6.2.1.1) (Acetate--CoA ligase) (Acyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACSA_SYNY3
Q55404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I., Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D., Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M., Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D., Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M. Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.; "Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=96127529; PubMed=8590279;
MEDLINE=96127529; PubMed=8590279;
MEDLINE=96127529; PubMed=8590279;
                                                                                                                                                                                                                                                                                         Synechocystis sp. (strain Bacteria; Cyanobacteria; C
                                                                                                                                                                                                                                                                                                                                              activating enzyme).
ACS OR SLL0542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Multigene family; Nuclear protein; Translation regulation CONFLICT 34 34 K -> N (IN REF. 1). SEQUENCE 189 AA; 21031 MW; 5E9B130584A75465 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U18408; AAC49047.1; -. EMBL; AC019018; AAG52268.1; -. EMBL; AF336915; AAG53996.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre European Bioinformatics Institute. There are no restricted the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: COULD ACT AS REGULATOR OF GENES RESPONSIBLE FOR MEDIATING THE VARIOUS AUXIN-INDUCED EVENTS RESPONSIBLE FO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.M., Toriumi M., Yu G., Brooks S., Chao Q Chen H., Karlin-Neumann G., Kim C., Lam B., Miranda M., Nguyen Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R.,
  region from map positions DNA Res. 2:153-166(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam;
                                                                                                                                                                                                                                                               NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003311; AUX_IAA.
Pfam; PF02309; AUX_IAA; 1.
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INDUCTION: BY AUXIN.
SIMILARITY: BELONGS TO THE AUX/IAA FAMILY.
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STRAIN-K12 / MG.655;
MEDLINE-95334362; PubMed-7610040;
MEDLINE-95334362; PubMed-7610040;
Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
Blattner F.R.;
Blattner F.R.;
"Analysis of the Escherichia coli genome VI: DNA sequenc region from 92.8 through 100 minutes.";
"Analysis of the Escherichia coli genome VI: DNA sequenc
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PROSITE: PS00455; AMP_BINDING; 1.

Ligase; Complete proteome.

SEQUENCE 653 AA
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P16688;
01-AUG-1990
01-NOV-1991
16-OCT-2001
PhnJ protein
Chen C.-M., Ye Q.-Z., Zhu Z., Wanner B.L., Walsh C.T.;

"Molecular biology of carbon-phosphorus bond cleavage. Cloning a sequencing of the phn (psil) genes involved in alkylphosphonate uptake and C-P Lyase activity in Escherichia coli B.";

J. Biol. Chem. 265:461-4471(1990).

J. FUNCTION: BELONGS TO AN OPERON INVOLVED IN ALKYLPHOSPHONATE UPTAKE AND C-P LYASE. EXACT FUNCTION NOT KNOWN.

-!- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF STRAIN K12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-91193228; PubMed-1840580; Makino K., Kim S.K., Shinagawa H., Amemura M., Nakata Makino K., Kim S.K., Shinagawa H., Amemura M., Nakata Makino K., Kim S.K., Shinagawa H., Amemura M., Nakata Makino K., Shinagawa H., Shinagawa H
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HSSP; P08659; 1LCI
Interpro; IPR000873; AMP-bind.
Pfam; PF00501; AMP-binding; 1.
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SIMILARITY: BELONGS
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PIR; B35719; B35719.

ECOGENC: EG10719; phnJ.

ECOGENC: EG10719; phnJ.

ECOMPLETE Proteome.

Alkylphosphonate uptake; Complete Proteome.

VARIANT 103 103 V -> L (IN STRAIN B)

VARIANT 281 AA; 31845 MW; 241F6AF140995468 C
                                                                                                                        Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T., "A 460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map. DNA Res. 3:379-392(1996).
                                                                                                                                                                                                                                                                                                                              STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P52007; P52008; P76295;
01-OCT-1996 (Rel. 34, C
15-JUL-1998 (Rel. 36, L
16-OCT-2001 (Rel. 40, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D90227; BAA14270.1; -. EMBL; U14003; AAA96997.1; -. EMBL; AE0000482; AAC77059.1; -. EMBL; J05260; AAA24348.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli.
Bacteria; Proteobacteria;
                                              Gupta S.D., Wu H.C.;
Submitted (FEB-1996)
                                                                                                                                                                                                                                                                                        STRAIN-KI
                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
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IDENTIFICATION BY MEDLINE=99420866;
                                                                           STRAIN-K12 /
                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                        MEDLINE=97251358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=562,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia
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                                                                                            OF 102-188
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                MASS
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   PubMed=10493123;
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No. 11;
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                                                                                                                                        linkage map.";
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SEQUENCE FROM N.A.
STRAIN-C57BL/6; TISSUE-Spleen;
STRAINE-98081836; PubMed-9419338;
MEDLINE-98081836; PubMed-9419338;
Hilton D.J., Richardson R.T., Alexander W.S., Viney E.M.,
Hilton D.J., Stari R., Nicholson S.E., Metc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WBS2_MOUSE STANDARD;
054929; Q9R1M8;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last seq
15-JUN-2002 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
EMBL;
        between
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Vasiliauskas D., Hancock
                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                        "Twenty proteins classes.";
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Electrophoresis 20:2181-2195(1999).
Electrophoresis 20:2181-2195(1999).
-!- SIMILARITY: STRONG, TO H.INFILUENZAE HI1582/HI1581.
-!- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
FRAMESHIFT IN POSITION 128 THAT PRODUCES TWO SEPARATE ORFS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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                                                                                                                                                                                                     "SWiP-1:
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                                                                                    SIMILARITY: CONTAINS 5
SIMILARITY: CONTAINS 1
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                             SWISS-PROT entry is
                                                                                                              P-1: novel SOCS box containing WD-protein res and by Shh during development.";
Dev. 82:79-94(1999).
IMILARITY: CONT.
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D90829; BAA15685.1; -
D90830; BAA15692.1; -
L38618; AAA89200.1; ALT_FRAME.
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and this statement is not removed.
requires a license agreement (See
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Rel. 41, Last annoctation updat
SOCS box containing protein 2
protein SWiP-2).
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thi; Muridae;
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DYR2_HUMAN
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Best Local
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REPEAT
DOMAIN
CONFLICT
                            Becker W., Joost H.-G.;
Submitted (NOV-1996) to the EMBL/GenBa
-i-FUNCTION: IN VITRO; CAN PHOSPHORYL
AND THR RESIDUES MAY BE INVOLVED
GROWTH AND/OR DEVELOPMENT.
                                                                                                            specificity of DYRK-related kinases,
specificity protein kinases.";
J. Biol. Chem. 273:25893-25902(1998).
                                                                                                                                                                                                                                                               Q92630;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Dual-specificity tyrosine-phosphorylation regulated kinase (EC 2.7.1.-).
  + + +
                                                                                                                                                      Becker W.,
Joost H.-G.
                                                                                TISSUE=Placenta;
                                                                                           SEQUENCE
                                                                                                                                                                          MEDLINE=98421512;
                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vo
Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                         DYRK2
                                                                                                                                                                                                                                                                                                                             DYR2_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00678; WD_REPEATS_1; 2.
PROSITE; PS50082; WD_REPEATS_2; 5.
PROSITE; PS50294; WD_REPEATS_REGION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00320; GPROTEINBRPT.
PTCDOM; PD000018; WH40; 2.
SMART; SM00253; SOCS; 1.
SMART; SM00320; WD40; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                 NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                        1 YDQDQMVVVQVPWP
SUBCELLULAR LOCATION: Cytoplasmic. PTM: AUTHOPHOSPHORYLATED ON TYR RESIMILARITY: BELONGS TO THE SER/THF
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Pro; IPR001680; WD40.
PF00400; WD40; 6.
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7; Conserv
                                                                                          OF 320-528
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Y., Wetzel K., Eirmbter
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PHOSPHORYLATE HISTONES H3 AND
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WD 2.
WD 3.
WD 4.
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  SER/THR
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No.
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                                         REGULATION
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RESULT 11
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ERG1_HUMAN STANDARD

Q14534; Q9UEK6;

Q1-NOV-1997 (Rel. 35, C

16-OCT-2001 (Rel. 40, L

16-OCT-2001 (Rel. 40, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S.TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP;
PROSITE; PS50011; PROTEIN_KINASE_DOM;
PROSITE; PS00108; PROTEIN_KINASE_ST; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                   inhibitors in HeLa cells.";
Biol. Chem. 271:8053-8056(1996).
J. Biol. Chem. 271:8053-8056(1996).
FUNCTION: CATALYZES THE FIRST OXYGENATION STEP IN STEROL
BIOSYNTHESIS AND IS SUGGESTED TO BE ONE OF THE RATE-LIMITING
ENZYMES IN THIS PATHWAY.
                                                                                                                                                                                                               SEQUENCE OF 187-535 FROM N.A.
                                                                                                                                                                                                                                                      "Localization of the squalene epoxidase chromosome region 8q24.1."; Genomics 44:141-143(1997).
                                                                                                                                                                                                                                                                                                                    Nagai M., Sakakibara J., Wakui K.,
Tsuji S., Arakawa M., Ono T.;
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-97432831; PubMed-9286711;
                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Squalene monooxygenase
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ATP-binding; Phosphorylation.
DOMAIN 149 462 PROTEIN KINASE.
DOMAIN 155 163 ATP (BY SIMILARIT)
BIND 155 163 ATP (BY SIMILARIT)
BINDING 178 178 ATP (BY SIMILARIT)
ACT_SITE 275 275 BY SIMILARITY.
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EMBL; Y09216; CAA70418.1; -.
HSSP; Q00534; 1B18.
Genew; HGNC:3093; DYRK2.
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                                                                                                                           Nakamura Y., Sakakibara J., Izumi T., Shibata A., "Transcriptional regulation of squalene epoxidase
                                                                                                                                                                       MEDLINE-96215195;
                                                                                                                                                                                               TISSUE-Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
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8; Conserv
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 (EC 1.14.99.7) (Squalene epoxidase) (SE)
  Squalene +
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Catarrhini; Hominidae
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  AH(2) +
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OR AYII_ARATH

OR P49677; O23312;

O1-FEB-1996 (Rel. 33, Created)

OT 01-FEB-1996 (Rel. 40, Last sequence update)

OT 16-OCT-2001 (Rel. 40, Last sequence update)

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                                  MEDLINE-20083488; PubMed-10617198;
Mayer K.F.X., Schueller C., Wambutt R.,
Pohl T., Duesterhoeft A., Stiekema W.,
                                                                                                                                                                                                                                                                                     MEDLINE-94105161; PubMed-8278386; Abel S., Oeller P.W., Theologis A.; "Early auxin-induced genes encode short-lived n Proc. Natl. Acad. Sci. U.S.A. 91:326-330(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eurosids II;
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        Harris B.,
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COFACTOR: FAD.
SUBUNIT: MAY FORM A COMPLEX WITH SQUALENE SYNTHASE.
SUBCELLULAR LOCATION: Microsomal.
SIMILARITY: BELONGS TO THE SQUALENE MONOOXYGENASE FAMILY.
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        Ansorge
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FAD (ADP PART) (PE -> G (IN REF. 2 PART) (PE -> PART) (PE -> PART) (PART) 
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Pred. No.
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tt R., Murphy G., Volckaert G., a W., Entian K.-D., Terryn N., Grivell L.A., Rieger M.,
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RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Post S., de Haan M., Maarse A.C., Schaefer M., Grimm M., Loehnert T.-H.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Piravandi E.,
RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
RA Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Prishman D., Hasse D., Lencke K., Mewes H.-W., Stocker S., Bielke C.,
RA Frishman D., Hasse D., Lencke K., Mewes H.-W., Stocker S.,
RA Erishman D., Hasse D., Lencke K., Mewes H.-W., Stocker S.,
RA Schnoh M., Murray J., Sheet P., Cordes M., Abour Threideh J.,
RA Schone M., Murray J., Sheet P., Cordes M., Abour Threideh J.,
RA Schone M., Murray J., Sheet P., Cordes M., Abour Threideh J.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Granat S., Schody N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA Chen E., Marra M., Martienssen R., McComble W.R.;
Thallana. T., Shah R.,
Ra Granat S., Scholas G., Chromosome 4 of the plant Arabidopsis
                                            Matches
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                                                                                                                                           Multigene family; Nuclear protein; Translation regulation CONFLICT 52 52 A \rightarrow T (IN REF. 1).
                                                                                                                                                                                 TRANSFAC; T04508; InterPro; IPR003311; AUX_IAA. Pfam; PF02309; AUX_IAA; 1.
                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vos P., Hoheisel J., Zimmermann
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SIMILARITY: BELONGS TO THE AUX/IAA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIATING THE VARIOUS
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    DQDQMVVVQVPW
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297336; CAB10235.1; -.
AL161539; CAB78498.1; -.
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NCTION: COULD ACT AS
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B., Portetelle D.,
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                                            Conservative
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                                                                                                                        19031 MW;
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AUXIN-INDUCED
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                                                             Pred.
                                                                              Score
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                                        Mismatches
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                                                           37;
                                                        DB
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AC P49678; O22596;

DY 01-FEB-1996 (Rel. 3), Created)

DY 01-FEB-1996 (Rel. 4), Last sequence update)

DY 01-FEB-1996 (Rel. 4), Last annotation update)

DY 15-JUN-2002 (Rel. 4), Last annotation update)

DY 15-JUN-2002 (Rel. 4), Last annotation update)

DE ANIAN-2002 (Rel. 4), Last annotation update)

DY 15-JUN-2002 (Rel. 4), Last annotation update)

DY 200-2003 (Rel. 4), Last annotation update)

DY 200-2
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Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Etqu P., Le

Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Etqu P., Le

Toriumi M., Yu G., Brooks S., Chao Q., Chen H., Karlin-Neumann R.

Kim C., Lam B., Miranda M., Nguyen M., Palm C.J., Shinn P.,

Southwick A., Davis R.W., Ecker J.R., Theologis A.;

"Full length cDNA of gene MXC7-6 (GI:9294192).";

Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: COULD ACT AS REGULATOR OF GENES RESPONSIBLE FOR

MEDIATING THE VARIOUS AUXIN-INDUCED EVENTS RESPONSIBLE FOR
                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20277480: PubMed=10819329;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu "Structural analysis of Arabidopsis thaliana chromc features of the regions of 4,504,864 bp covered by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=cv. Wassilewskija;
Malik M.K., Zimmerman J.L.;
"Molecular characterization of a genomic clone
inducible IAA2 gene from Arabidopsis thaliana."
(In) Plant Gene Register PGR97-178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-cv. Columbia;
MEDLINE-94105161; PubMed-8278386;
Abel S., Oeller P.W., Theologis A.;
"Early auxin-induced genes encode short-lived nuclear Proc. Natl. Acad. Sci. U.S.A. 91:326-330(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
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            Translation regulation
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             AXI4_ARATH
P33077;
01-OCT-1993
01-NOV-1995
15-JUN-2002
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SEQUENCE
                                                                                                                                                                                                                                      InterPro: IPR03311; AUX_IAA.
Pfam; PF02309; AUX_IAA; 1.
Multigene family; Nuclear protein;
SEQUENCE 179 AA; 20330 MW; 0D21
                                                                                                                                                                                                                                                                                                                                 the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-94016594; PubMed-8411182;
Octler P.W., Keller J.A., Parks J.E., Silbert J.E., Theologis A.;
"Structural characterization of the early indoleacetic acid-inducible genes, PS-IAA4/5 and PS-IAA6, of pea (Pisum sativum L.).";
J. MOI. Biol. 233:789-798(1993).
-i- FUNCTION: COULD ACT AS RECULATOR OF GENES RESPONSIBLE FOR MEDIATING THE VARIOUS AUXIN-INDUCED EVENTS RESPONSIBLE FOR CELL
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  Auxin-responsive
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                                                                                                                                                                                      Similarity 58.:
7; Conservative
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174 AA;
               (Rel. 27, Created)
(Rel. 32, Last seq
(Rel. 41, Last ann
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19910 MW;
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ein IAA4 (Indoleacetic a
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1; Mismatches
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DECA4F59F0106179 CRC64;
                                                                                                                                                                                                                                       ein; Translation regulation OD212F384D100D7E CRC64;
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Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Etgu P. Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Etgu P. Toriumi M., Yu G., Brooks S., Chao Q., Chen H., Karlin-Neum Kim C., Lam B., Miranda M., Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R., Theologis A.;
Full length CDNA of gene MQD19.3 (G1:1017998).";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: COULD ACT AS REGULATOR OF GENES RESPONSIBLE F MEDIATING THE VARIOUS AUXIN-INDUCED EVENTS RESPONSIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=91338700; PubMed=2102379;
Conner T.W., Goekjian V.H., Lafayette P.R.,
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IAA4 OR AUX2-11 OR AT5C43700 OR MOD19.3.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheol Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                InterPro: IPRO03311; AUX_IAA.

Pfam; PF02309; AUX_IAA; 1.

Multigene family; Nuclear protein;
SEQUENCE 186 AA; 20975 MW; DCF6
                                                                                                                                                                                                                                                                                                                   EMBL;
PIR; (
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TRANSFAC; T04511; -.
InterPro; IPR003311;
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EMBL; L15450; AAA16571.1; -.
EMBL; AB026651; BAB11297.1; -.
EMBL; AF332394; AAG48758.1; -.
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Kaneko T., Katoh T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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149
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SIMILARITY: BELONGS TO THE AUX/IAA FAMILY.
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DGDWMLVGDVPW 160
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O9c8n7 arabidopsis
O9lqe8 arabidopsis
O9lqe8 arabidopsis
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## ALIGNMENTS

RESULT 1 Q9ZT62

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RESULT
Q9FND9
ID Q9
AC Q9
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Best Local S
Matches 14
Q9FND9;
Q9FND9;
01-MAR-2001
01-MAR-2001
01-JUN-2002
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O9ZT62:

OPZT62:

O1-MAY-1999 (TrEMBLrel. 10, Created)

O1-MAY-1999 (TrEMBLrel. 10, Last sequence update)

O1-MAY-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                              TISSUE-LEAF;
Ohsumi C., Nozaki J., Kida T.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF073744; AAD02832.1; -.
Glycosyltransferase; Transferase.
SEQUENCE 784 AA; 86920 MW; 3B06A491F0908933 CRC64;
                                                                                                                                                                                                                                                                                                                           Cucumis sativus (Cucumber).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
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Last annotation update)
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Pred. No. 6.4e-06;
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Best Local S
Matches 8
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Q9LQE3;
01-OCT-2000
                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core «
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tabata S.; "Structural analysis of Arabidopsis thaliana chromosome 5. sequence features of the regions of 1,044,062 bp covered b physically assigned P1 clones."; DNA Res. 4:291-300(1997).
 SEQUENCE FROM N. Cheuk R., Shinn
                                       Submitted
                                                                                          Submitted
                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                       01-JUN-2002
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Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
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                                                 Ecker J
                                                               SEQUENCE FROM
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid

eurosids_II; Brassicales; Brassicaceae; Arabidopsis.
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MEDLINE=98069011; PubMed=9405937;
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Pred. No. 2.6;
2; Mismatches 1
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 Buehler
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Best Local
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Q9C5W8;
01-JUN-2001
01-JUN-2001
01-DEC-2001
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Q38832;
Q1-NOV-1996
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Lee J., Lenz C., Li J
Nguyen M., Palm C., H
Thaveri A., Toriumi N
                                                     Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotytedons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsk
Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Sou
Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Fe
Theologis A., Ecker J.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC007887; AAF79366.1; -.
InterPro; IPR003340; TF_B3.
SEQUENCE
                               NCBI_TaxID=3702;
                                                                                                                                                            IAA14
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01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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Schwartz J., Southwick A.
G., Davis R., Federspiel
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Howing B.,
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Q9XID4;
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01-NOV-1999 (TrEMBLrel. 1
01-NOV-1999 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
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O23311;
O1-JAN-1998
F23M19.4 protein.
F23M19.4.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1998 (TrEMBLrel. 05, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
IAA7-like protein (IAA7 like protein).
DL3315C OR A74G14550.
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EMBL; AL161539; CAB78497.1; --
EMBL; AL161539; CAB78497.1; --
EMBL; AL161539; CAB78497.1; --
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Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Goldsmith A.D., Lee J.M., Toriumi M., Yu G., Bar
Chen H., Karlin-Neumann G., Kim C., Lam B., Mix
Palm C.J., Shinn P., Southwick A., Davis R.W.,
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NCE 228 AA; 25044 MW;
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NCE 234 AA; 2568
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8; Conserv
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Thim1 M., Yu G., Brooks S.
Broker
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ne EMBL/GenBank/DDBJ
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5.7;
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                   Embryophyta; Tracheophyta;
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s S., Chao
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InterPro; IPR00359; LRR_out.
Pfam; PF00560; LRR; 7.
Pfam; PF00069; pkinase; 1.
PRINTS; PR00019; LEURICHRPT.
PRODOm; PD000001; EUk_pkinase; 1.
SMART; SM00370; LRR; 6.
SMART; SM00370; LRR; 6.
ATP-binding; Hypothetical protein; Transferase, ATP-binding; Hypothetical protein; Transferase, SEQUENCE 719 AA; 77329 MW; 3B91891A64E0DFD3 C:
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation updat
Hypothetical 77.3 kDa protein.
F18021_60.
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EMBL; AC007454; AAD39615.1; -.
InterPro; IPR003311; AUX_IAA.
InterPro; IPR003340; TF_B3.
Pfam; PF02309; AUX_IAA; 1.
Pfam; PF02362; B3; 1.
SEQUENCE 619 AA; 69995 MW; 1DA4DD7BC43927E7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis
                                                                                                                                                                                                                                                                                                                                                           EU Arabidopsis sequencing project;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AL163763; CAB87409.1; -
InterPro; IPR000719; Euk_Pkinase.
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Lemcke K., Mayer K.F.X.,
Submitted (APR-2000) to 1
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STRAIN-CV. COLUMBIA;
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                          55.0%;
54.5%;
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., Quetier F., Salanoubat M.;
o the EMBL/GenBank/DDBJ databases.
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Score 44; DB Pred. No. 19; 4; Mismatches
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MEDILINE-21608550; PubMed=11743193;
MEDILINE-21608550; PubMed=11743193;
Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Ruymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
                                                                                                                                                                                                                                                                                                 Q8UJB3
Q8UJB3;
                                                                                                                                                                                           Agrobacterium tumefaciens (strain C58 / ATCC Bacteria; Proteobacteria; alpha subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2001 (TrEMBLrel. 01-OCT-2001 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.
                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21082930; PubMed=11214968; Kato T., Sasan Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasan Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A. Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimot Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                 Rhizobiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
DNA Res. 7:331-338(4691.1; -.
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InterPro; IPR002104; Phage_integrase.
Pfom; PF00589; Phage_integrase; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
Plasmid; Complete proteome.
SEQUENCE 416 AA; 46416 MW; 1DAB19
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Rhizobiaceae
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RESULT 12 Q8S3B5 ID Q8S3B AC Q8S3B

Q8S3B5 Q8S3B5;

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O81350;
O81350;
O1-NOV-1998 (TrEMBLrel. 08, Created)
O1-NOV-1998 (TrEMBLrel. 08, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
5'-adenyly!sulfate reductase (EC 1 8.99)
5'-adenyly!sulfate reductase (Hollow green seaweed).
                                                                                                                                     macroalga Enteromorpha intestinalis.";

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases

EMBL; AF069951; AAC26855.1;

InterPro; IFR004508; APS_reduc.

InterPro; IFR002500; PAPS_reduct.

InterPro; IFR000635; Thiored.

Pfam; PF01507; PAPS_reduct; 1.

pfam; PF00085; thiored; 1.

PRINTS; PR00421; THIOREDOXIN.
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Gao Y., Leustek T.;
"Cloning of 5'-adenylylsulfate (APS) reductase from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science [2]
                                                                                                  Oxidoreductase.
SEQUENCE 423 AA;
                                                                                                                                                                                                                                                                                                             Enteromorpha.
NCBI_TaxID=3116;
                                                                                                                                                                                                                                                                                                                                       Enteromorpha intestinalis (Hollow green seaweed).
Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Ulvales; Ulvaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of the plant Agrobacterium tumefaciens C58 Science 294:2323-2328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin Houmiel K., Gordon J., Yaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz Wollam C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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MEDLINE=21608551; PubMed=11743194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The genome C58.";
                                                                                                                             TIGRFAMS; TIGR00424;
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                                                   Conservative
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58.3%;
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87.5%;
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Pred. No.
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                                                                                                    808EE4F3BD56F1F2
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039281;
01-JAN-1998
01-JAN-1998
01-JUN-2002
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Phaseolus lunatus (Lima bean) (Phaseolus limensis).

Phaseolus lunatus (Lima bean) (Phaseolus limensis).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
                                                                           Telford E.A., Watson M.S., Perry J., Cullinand Submitted (OCT-1997) to the EMBL/GenBank/DDBJ EMBL; AF030027; AAC59558.1; -. InterPro; IPR004936; Herpes_UL21. Pfam; PF03252; UL21; 1. SEQUENCE 529 AA; 58150 MW; E2B737B89D48941
                                                                                                                                                                MEDLINE-98264497; PubMed-9603335;
Telford E.A., Watson M.S., Perry J., Cullinar
"The DNA sequence of equine herpesvirus-4.";
J. Gen. Virol. 79:1197-1203(1998).
                                                                                                                                                                                                                                               the
                                                                                                                                                                                                                                                        "The
                                                                                                                                                                                                                                                                   Nicolson
                                                                                                                                                                                                                                                                                                                          Viruses; dsDNA viruses, no RNA stage;
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                              Equine herpesvirus 4.
                                                                                                                                                                                                                                                                                                                                                                 Counterpart
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Shan X., Martin R.C., Mok D.W.S., Mok M.C.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AF489877; AAM09517.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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283
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                  DOMVVVQVPWP 14
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 DEIILVEEPWP
                                      Similarity
5; Conserv
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7; Conser
                                                                                                                                                                                                                                    Virol.
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                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 05, Created)
(TrEMBLrel. 05, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
of HSV-1 gene UL21 and VZV gene 38.
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                                       Conservative
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45.5%;
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                                     Score 42; DB Pred. No. 32; 5; Mismatches
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                                                       Length 529;
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AMEDLINE-2010f579; Pubmed=11130712;
AN Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
AN White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
AN White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
AN Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
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AN Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
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AN Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
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AN Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
AN AN Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
AN AN MILITSCHET J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
AN AN MILITSCHET J., Van Aken S., Vaysberg M., Vsottkala V.S., Walker M.,
Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

"Sequence and analysis of chromosome l of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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01-JUN-2001
01-JUN-2002
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01-OCT-2000
01-OCT-2000
01-JUN-2002
                                          SEQUENCE F
Ecker J.R.
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                                                                                                                                                       Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embry.
Spermatophyta; Magnollophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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InterPro; IPR003340; TF_B3.
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EMBL; AC023913; AAG51894.1;
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NCE 600 AA; 67933 MW;
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RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

RI Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

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RA Cheuk R., Sakan R., Hansen R., Khin Q., Johnson R., Khin Q., J
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80
1 YDQDQMVVVAVA
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US-09-754-853A-1101

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De 114, Appl 1103, Ap 11113, Ap 11115, Ap 11110, Ap 11110, Ap 11112, Ap 11109, Ap 1110
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US-09-738-626-3614	US-09-943-689A-2	US-09-925-300-1320	US-09-943-689A-4	US-09-815-242-10944	US-09-975-719-265	US-09-950-933A-66	US-09-893-817-8	US-09-893-817-4	US-10-008-739A-2	US-09-987-025-2	US-09-923-556-6	US-09-923-556-2	US-10-047-412A-29	US-10-047-412A-10	US-09-997-267-2	US-09-997-267-4	US-09-885-827-1	US-09-281-717-50	US-10-029-495-5	US-09-922-217-1107	US-10-025-380-1107	US-09-855-154-2	US-09-908-805B-21	US-09-754-853A-1108	US-09-754-853A-1106
Sequence 3614, Ap	$\sim$	Sequence 1320, Ap	Sequence 4, Appli	Sequence 10944, A	Sequence 265, App	Sequence 66, Appl	Sequence 8, Appli	Sequence 4, Appli	~	Sequence 2, Appli	6,	۵ ۲	Sequence 29, Appl	Sequence 10, Appl	Sequence 2, Appli	Sequence 4, Appli	Sequence 1, Appli	Sequence 50, Appl	Sequence 5, Appli	Sequence 1107, Ap	Sequence 1107, Ap	Sequence 2, Appli	Sequence 21, Appl	Sequence 1108, Ap	Sequence 1106, Ap

## ALIGNMENTS

RESULT 1 US-09-772-134B-14

GENERAL INFORMATION:

Patent No. US20020144310A1

Application US/09772134B

Sequence 14,

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US-09-754-853A-1103
; Sequence 1103, Application US/09754853A
; Publication No. US20030005491A1
; GENERAL INFORMATION:
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; EEATURE;
; NAME/KEY: misc_feature
; LOCATION: (1)..(830)
; OTHER INFORMATION: Xaa is any amino acid
US-09-772-134B-14
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SEQ ID NO 14
LENCTH: 830
TYPE: PRT
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Best Local Similarity
Matches 6; Conserv
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APPLICANT: Lightfoot, David
APPLICANT: Lightfoot, David
APPLICANT: Lightfoot, David
APPLICANT: Meksem, Khalid
TITLE OF INVENTION: ISOLATED POLYNUCLEOTIDES AND POLYPEPTIDES RELATING TO LOCI UND
TITLE OF INVENTION: RESISTANCE TO SOYBEAN CYST NEMATODE AND SOYBEAN SUDDEN DEATH
TITLE OF INVENTION: METHODS EMPLOYING SAME
FILLE REFERENCE: 1268/4/2
CURRENT APPLICATION NUMBER: US/09/772,134B
CURRENT FILING DATE: 2001-01-28
PRIOR APPLICATION NUMBER: 60/178,811
PRIOR FILING DATE: 2000-01-28
NUMBER OF SEQ ID NOS: 122
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; OTHER INFORMATION: Clone ID: rhgl_peking_amplicon
US-09-754-853A-1103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 1119
SEQ ID NO 1105
LENGTH: 854
TYPE: PRT
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                                  APPLICANT: Hauge, Brian M.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
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APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
FILE REFERENCE: 38-10(15810)B
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
                    APPLICANT:
APPLICANT:
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APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
FILE REFERENCE: 38-10(15810)B
TITLE
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APPLICANT: Parnel
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APPLICANT: Parnell, Laure
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OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
                    Wang, Ming Li
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Pred. No.
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Best Local Similarity
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                                                                                                                                                                      Sequence 1115, Application US/09754853A Publication No. US20030005491A1 GENERAL INFORMATION:
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SEQ ID NO 1113
LENGTH: 854
TYPE: PRT
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SEQ ID NO 1111
LENGTH: 854
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APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules
TITLE OF INVENTION: Soybean Cyst Nematode
FILE REFERENCE: 38-10(15810)B
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
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APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
FILE REFERENCE: 38-10(15810)B
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APPLICANT: Parnel
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PRIOR FILING DATE: 2000-01-07
NUMBER OF FOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
FILE REFERENCE: 38-10(15810)B
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 1119
SEQ ID NO 1104
LENGTH: 877
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APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
FILE REFERENCE: 38-10(15810)B
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION UMBER: US 60/174,880
PRIOR PELING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 1119
SEQ ID NO 1102
LENGTH: 877
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
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US-09-754-853A-1115
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NUMBER OF SEQ ID NOS: 1119
SEQ ID NO 1115
LENGTH: 854
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Best Local Similarity 54.5%;
Matches 6; Conservative
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Best Local :
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54.5%;
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Pred. No. 11;
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APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And
TITLE OF INVENTION: Soybean Cyst Nematode Re:
FILE REFERENCE: 38-10(15810)B
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEO ID NOS: 1119
SEO ID NO 1112
SEO ID NO 1112
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US-09-754-853A-1112
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US-09-754-853A-1112
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CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 1119
SEQ ID NO 1110
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Best Local S
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Best Local :
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APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
FILE REFERENCE: 38-10(15810)B
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APPLICANT: Parnell, Laurer
APPLICANT: Parsons, Jerem
APPLICANT: Wang, Ming Li
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                                     ORGANISM: Glycine max FEATURE:
                                                                                   TYPE: PRT
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TYPE: PRT
               OTHER INFORMATION: Clone ID: rhgl_lee_amplicon
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Local Similarity 54.5%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 9; Length 877; Pred. No. 11;
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PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 1119
SEQ ID NO 1114
LENGTH: 877
TYPE: PRT
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TITLE OF INVENTION: Nucleic Acid Molecules
TITLE OF INVENTION: Soybean Cyst Nematode
FILE REFERENCE: 38-10(15810)B
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
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                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
                                                                                                                                                                                                                                                                                                                            APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Acomica-X-1

CHEDINE AND THE REFERENCE: Acomica-X-1
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                                                                                                         APPLICATION NUMBER: US 60/236,359 FILING DATE: 2000-09-27
                                                                                                                                        FILING DATE: 2000-08-03
APPLICATION NUMBER: GB 24263.6
FILING DATE: 2000-10-04
                                                                     APPLICATION NUMBER: PCT/US01/00666 FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664 FILING DATE: 2001-01-30
                                  FILING DATE:
                                                   APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
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Pred. No.
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ORGANISM:
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US-09-798-889-50
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SOFTWARE: Pa
SEQ ID NO 50
LENGTH: 46
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Best Local
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LENGTH: 90
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TITLE OF INVENTION: 31 Human secreted proteins
FILE REFERENCE: P2026P1
FILE REFERENCE: P2026P1
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                                                                                    PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PRIOR FILING DATE: 1998-03-12
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-09
                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/798,889
CURRENT FILING DATE: 2001-03-06
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NUMBER OF SEQ ID NOS: 49117
                                                                 NUMBER OF SEQ ID NOS: 185
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APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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APPLICATION NUMBER: PCT/US01/00661
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APPLICATION NUMBER: PCT/US01/00662
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EXPRESSED IN BRAIN, SIGNAL = 1.5
EXPRESSED IN ADULT LIVER, SIGNAL = 3.5
EXPRESSED IN LONG, SIGNAL = 2.2
EXPRESSED IN BONE MARROW, SIGNAL = 1.2
EXPRESSED IN BONE MARROW, SIGNAL = 1.4
EXPRESSED IN PLACENTA, SIGNAL = 1.7
EXPRESSED IN HELA, SIGNAL = 1.7
EXT_HUMAN HIT: AM962016.1, EVALUE 2.00e-23
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Pred. No.
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APPLICANT: Hauge, Brian M.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
APPLICANT: Wang, Ming Li
ITILE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
ITILE OF INVENTION: Soybean Cyst Nematode Resistance
FILE REFERENCE: 38-10(15810)8
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 1119
SEQ ID NO 1098
LENGTH: 854
TYPE: PRT
ORGANISM: Glycine max
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NAME/KEY: SITE
; LOCATION: (46)
; OTHER INFORMATION: Xaa equals stop translation
US-09-798-889-50
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Sequence 1101, Application US/09754853A
PUBLICATION NO. US20030005491A1
GENERAL INFORMATION:
APPLICANT: Hauge, Brian M.
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THER INFORMATION: Clone ID: 240017_region_G3
US-09-754-853A-1098
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; OTHER INFORMATION: Clone ID: rhgl_A3244_amplicon US-09-754-853A-1101
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US-09-754-853A-1098
                                                                         APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
FILE REFERENCE: 38-10(15810)B
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR FILING DATE: 2000-0107
NUMBER OF SEQ ID NOS: 1119
SEQ ID NO 1101
LENGTH: 854
TYPE: PRT
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Best Local Similarity bo.,
"""hes 6; Conservative
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Best Local Similarity 55.0
Conservative
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                                     ORGANISM: Glycine max FEATURE:
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Pred. No. 2.
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Query Match 50.0%; Score 40; DB 9; Length 854;
Best Local Similarity 55.6%; Pred. No. 52;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps

Qy 5 QMVVVQVPW 13
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Db 117 QVIVIQLPW 125
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Search completed: March 27, 2003, 10:20:37 Job time :  $4.2439 \ \text{secs}$ 

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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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3: /cgn2_6/ptodata/1/laa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*

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   PVSVGCFVGFDASEPDSRH
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US-08-946-234-5
US-08-965-223-450
US-08-861-774E-22
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US-09-105-697-5
US-09-105-697-6
US-09-105-997-434-10
US-08-254-359A-6
US-08-458-359A-6
US-08-458-313-31
US-08-458-8119-10
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	Query M Best Lo Matches	ATT N R R TEL	C CORNO CON CON CONTRACTOR	COR	Patent No GENERAL APPLIC, APPLIC, APPLIC, TITLE ( TITLE (	RESULT 1 US-08-846	200 200 200 200 200 200 200 200 200 200
1 PVSV(      1 PVSV(	atcl cal	ATTORNEY/AGENT INFORMATION: NAME: NORMAN F. OBLON REGISTRATION NUMBER: 24,618 TELECOMMUNICATION INFORMATION: TELEPHONE: (703)-413-3200 TELEFAX: (703)-413-2220 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 19 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: peptide FRAGMENT TYPE: internal S-08-846-234-2	COUNTRY: USA  ZIP: 22202  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compat! OPERATING SYSTEM: PC-DOS SOFTMARE: Patentin Relea CURRENT APPLICATION DATA: APPLICATION NUMBER: US/OFFILING DATE:	RRESPONDENC ADDRESSEE: STREET: 1: CITY: ARL:	MEENT NO. 6166292 ENERAL INFORMATION: ENERAL INFORMATION: APPLICANT: OSUMI Chi APPLICANT: NUZAKI Ji APPLICANT: KIDA Taka TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:	2 3	39.5.5400 39.400 39.5.5400 39.5.5400
PVSVGCFVGFDAS             PVSVGCFVGFDAS	h Similarity 19; Conse	'AGENT I NORMAN NORMAN NORMAN NORICATION NE: (703 NE: (703 NE) NOR SEE CHARACT 19 am amino a amino a ariy: lin ary: lin Type: Type:	YINGIN USA 2202 2202 READABL IYPE: IBM R: IBM RS YST E: Pat PPLICAT FION NU DATE:	DENCE A EE: OB 1755 ARLINGT	INFORMATION ANT: OSUMI ANT: NOZAK ANT: KIDA ANTI KIDA OF INVENTIO OF INVENTIO	) Applica	38.1 38.1 38.1 38.1 37.6 37.1 37.1 37.1 37.1
PVSVGCFVGFDASEPDSRH              VSVGCFVGFDASEPDSRH	cvat	T INFORMATION: AN F. OBLON AN UMBER: 24, TION INFORMATI (703)-413-3220 703)-413-2220 SEQ ID NO: 2 ACTERISTICS: amino acids o acid linear inpeptide :: peptide	ISA ABBLE FORM: ABBLE FORM: I Floppy disk IIBM PC compatible FYSTEM: PC-DOS/MS Patentin Release CATION DATA: CATION DATA: INUMBER: US/08/8	ADDRESS: OBLON, SP S S. JEFF	7292 ATTION: ATTION: COSUMI Chieko NOZAKI Jinshi KIDA Takao TENTION: RAFF ENTION: PROD	tion US	833 8334 8334 8333 8333 8333 8333 8333
RH 19 	100.0%; 100.0%; ive	TION: DN 4,6 24,6 3-3000 3-3000 3-2220 2:2220 CS: ids	: disk npatible C-DOS/MS Release FA: US/08/8	RESS: N, SPIVAK, JEFFERSON	INC	/0884	44500000440400001444
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	core 105; I red. No. 2e Mismatches		, Version	LLAND, M HIGHWAY	SYNTHASE GI RAFFINOSE,	ALIGNMENTS	US-09-350-309-6 US-08-520-946-6 PCT-US91-07035-8 PCT-US91-1418-2 PCT-US95-15327-2 US-08-338-530A-2 US-08-38-536-244-3 US-08-843-659-4 PCT-US95-14418-4 PCT-US95-14418-4 PCT-US95-14418-4 PCT-US95-14418-4 PCT-US95-14418-4 PCT-US95-14418-4 PCT-US95-14418-4 PCT-US95-14418-4 US-08-073-384C-8 US-08-08-254-359A-8 US-08-481-238-8
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GENERAL INFORMATION:
APPLICANT: OSUMI Chieko
APPLICANT: NOZAKI Jinshi
APPLICANT: KIDA 7222-
TITI.F
                                                                                                                                                                                                                                                                                                                                                                                         US-08-905-223-460
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Best Local Similarity
Matches 19; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                  APPLICANT: Edwarus,
APPLICANT: Duelert, Aymeric
APPLICANT: Lacroix, Bruno
APPLICANT: Lacroix, Bruno
TANVENTION: 5' ESTS FOR SECRETED PROTEINS
                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95
                SOFTWARE: Word
CURRENT APPLICATION DATA:
                                                                                                                                                                                         NUMBER OF SEQUENCES: 503
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 501 West Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (703)-413-3000
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NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: RAFFINOSE SYNTHASE GENE, METHOD FOR TITLE OF INVENTION: PRODUCING RAFFINOSE, AND TRANSGENIC PLANT NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR CITY: ARLINOTON
STATE: VIRGINIA
                                                                                                                                                     STREET: 501 West I
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 PVSVGCFVGFDASEPDSRH 79
APPLICATION NUMBER:
                                                                                                                        ZIP: 92101-3505
                                                                                                                                      COUNTRY:
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ZIP: 22202
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(703)-413-2220
TD NO: 5:
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Pred. No. 1.2e-08;
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                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/08/861,774E
CURRENT FILING DATE: 1997-05-22

NUMBER OF SEQ ID NOS: 94
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22
LENGTH: 212
TYPE: PRT
                                                        Best Local Similarity Matches 7; Conserv
                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 36. Matches 7; Conservative
                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: METHOD FOR ISOLATION OF BIOSYNTHESIS GENES FOR TITLE OF INVENTION: BIOACTIVE MOLECULES
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Waters, Barbara
APPLICANT: Miao, Vivian
APPLICANT: Ho, Yap
APPLICANT: Tong, Seow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (619) 235-017
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                             NAME/KEY: SITE LOCATION: (136)
OTHER INFORMATION: Xaa=unknown amino acid
                                                                                                                                                                            FEATURE:
                                                                                                                                                                                       ORGANISM: Xanthoparmelia cumberlandia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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IDENTIFICATION METHOD:
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LOCATION: -17..-1
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Tong, Se
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                                                          Conservative
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36.8%;
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                                                          Mismatches
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                                                                                    Length 212;
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                                                          Indels
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RESULT 5 US-08-861-774E-34 ; Sequence 34, Application US/08861774E

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APPLICANT: Miao, Vivian
APPLICANT: Ho, Yap
APPLICANT: Tong, Seow
ITITLE OF INVENTION: METHOD FOR ISOLATION OF BIOSYNTHESIS GENES FOR
ITITLE OF INVENTION: BIOACTIVE MCLECULES
ITITLE OF INVENTION NUMBER: US/08/861,774E
CURRENT APPLICATION NUMBER: US/08/861,774E
CURRENT FILING DATE: 1997-05-22
NUMBER OF SEO ID NOS: 94
SOFTWARE: Patentin Ver. 2.0
SEO ID NO 34
LENCTH: 212
TYPE: PRT
ORGANISM: Leptoglum corniculatum
US-08-861-774E-34

39.0%: Score 41: DB 4: Length 212:
                                                                       ; MOLECULE TYPE: US-09-105-697-4
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Best Local Similarity 43.8%;
Matches 7; Conservative
Best Local Similarity 61.5
Matches 8; Conservative
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                                Query Match
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                                                                                                                                                                                                     TELEFAX: (510)814-2977
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Waters, Barban
APPLICANT: Miao, Vivian
                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Petry Ph.D., Douglas A.
REGISTATION NUMBER: 35321
REFERENCE/DOCKET NUMBER: 1043
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510)814-2974
                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Rclease #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gelfand Ph.D., David H.
APPLICANT: Reichert, Fred L.
TITLE OF INVENTION: MUTANT CHIMERIC DNA POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 PEDVGCYIGACATDYD 37
                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Roche Molecular Systems STREET: 1080 U.S. Highway 202
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/105,697
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                                                                                      protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                 38.1%;
0; Mismatches
                 Score 40; DB Pred. No. 75;
                                                                                                                                                                                                                                                                              1043
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                                  4.
                              Length 291;
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Gaps
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US-09-105-697-5
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                                                                                                                                                                                                                                   Sequence 6, Applica
Patent No. 6228628
                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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APPLICANT: Gelfand Ph.D., Da
APPLICANT: Reichert, Fred L.
                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Petry Ph.D., Douglas A.
REGISTRATION NUMBER: 35321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                 APPLICANT: Gelfand Ph.D., David H.
APPLICANT: Reichert, Fred L.
TITLE OF INVENTION: MUTANT CHIMERIC DNA POLYMERASE
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (510)814-2974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                             STREET: 1080 U.S. CITY: Branchburg STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                               38.1%;
Local Similarity 61.5%;
les 8; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1080 U.S. CITY: Branchburg STATE: New Jersey
                                      ZIP: 08876
                                               COUNTRY:
                                                                                              ADDRESSEE: Roche Molecular Systems
STREET: 1080 U.S. Highway 202
                                                                                                                                                                                                                                                                                                                                         64 FVVFDAKAPSFRH 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sir
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1080 U.S. Highway 202
                                                  United States
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
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                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40; DB
Pred. No. 75;
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RESULT 9
US-07-977-434-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMER: US 590,490
FILING DATE: 28-SEP-1990
PRIOR APPLICATION NUMBER: US 590,466
APPLICATION NUMBER: US 590,466
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                            COMPUTER: Macintosh
OPERATING SYSTEM: 7
SOFTWARE: WordPerfect 2.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07,
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gelfand, David H. APPLICANT: Abramson, Richard TITLE OF INVENTION: 5, TO 3, TITLE OF INVENTION: THERMOST
                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (510)814-2974
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NAME: Petry Ph.D., Douglas A.
REGISTRATION NUMBER: 35321
                                                                                                            PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                      APPLICATION NUMBER: US 523,394 FILING DATE: 15-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 291 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                           APPLICATION NUMBER: US 5 FILING DATE: 28-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 FVVFDAKAPSFRH 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.1%; Local Similarity 61.5%; es 8; Conservative
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New Jersey ZIP: 07110-1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Nutley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (510)814-2977
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12-JAN-1988
ON DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n, Richard D.
5' TO 3' EXONUCLEASE MUTATIONS
THERMOSTABLE DNA POLYMERASES
                                    US 143,441
                                                                                                                                            us 590,213
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 291;
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RESULT 10
US-07-977-434-10
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APPLICANT: Gelfand, David H.
APPLICANT: Abramson, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (510) 814-2972 INFORMATION FOR SEQ ID NO: 8:
                                                                                COMPUTER: Macintosh
OPERATING SYSTEM: 7
SOFTWARE: WordPerfect 2.1
CURRENT APPLICATION DATA:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: Case No. 5466591 8753
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 24-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Luann Cserr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 0
FILING DATE: 22-DEC-
PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                    ADDRESSEE:
STREET: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38.1%;
Local Similarity 61.5%;
nes 8; Conservativo
                                                    APPLICATION NUMBER: US/07/977,434 FILING DATE:
                                                                                                                                                                                         STATE: New Jersey ZIP: 07110-1199
                                                                                                                                                                                                                          CITY: Nutley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 FVVFDAKAPSFRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 609,157 FILING DATE: 02-NOV-1990
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24-JUL-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JMBER: US 063,509
17-JUN-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-DEC-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76
                                                                                                                                                                                                                                                                                                        THERMOSTABLE DNA POLYMERASES
                                                                                                                                                                                                                                                                                                                        , Richard D.
5' TO 3' EXONUCLEASE MUTATIONS
   US 590,490
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28-SEP-1990

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                                                                                                                                Sequence 6, Application US/08073384C Patent No. 5541311 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 24-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Luenn Cserr
REGISTBARTON.
                             TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                             APPLICANT: Dahlberg, James E. APPLICANT: Lyamichev, Victor I. APPLICANT: Brow, Mary Ann D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 834 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (510) 814-2972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 17 FILING DATE: 02-NOV-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 20-SEP-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 746,121 FILING DATE: 15-AUG-1991 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 15-MAY-PRIOR APPLICATION DATA:
                 CORRESPONDENCE ADDRESS
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                       64 FVVFDAKAPSFRH 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: Case No. 5466591 8753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 8:
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FILING DATE: 12-JAN-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 5 FILING DATE: 28-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: WO PCT/US90/07641 FILING DATE: 21-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
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                                                                                                                                                                                                                                                                                 7 FVGFDASEPDSRH 19
                                                                                                                                                                                                                                                                                                                      Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                      Conservative
HAVERSTOCK, MEDLEN & CARROLL
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20-SEP-1990
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                                   POLYMERASE
29
                                                                SYNTHESIS-DEFICIENT THERMOSTABLE DNA
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                                                                                                                                                                                                                                                                                                                                        .4e+02;
                                                                                                                                                                                                                                                                                                                      5; Indels
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US-08-254-359A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: DAHLBERG, JAMES E.
APPLICANT: LYAMICHEV, VICTOR I.
APPLICANT: BROW, MARY ANN D.
TITLE OF INVENTION: 5' NUCLESSES DERI
TITLE OF INVENTION: DNA POLYMERASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:
MEDIEN & CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/254,359A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07 FILING DATE: 07-DEC-1992 ATTORNEY/AGENT INFORMATION: NAME: Carroll, Peter G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: FO TELECOMMUNICATION INFORMATION: 415/705-8410
                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,384
FILING DATE: 06-JUN-1993
                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: Unit:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                 ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL STREET: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IIBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COUTHABER: ACTUAL STATEMENT PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 220 CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 FVVFDAKAPSERH 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/01 FILING DATE: 04-JUN-1993
                                                                         CLASSIFICATION: 435
                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                     STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 FVGFDASEPDSRH 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n 38.1%;
Similarity 61.5%;
8; Conservative
                                                                                                                                                                                                                                                 94104
                                                                                                                                                                                                                                                                                     CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                      LYAMICHEV, VICTOR I.
BROW, MARY ANN D.
VENTION: 5' NUCLEASES DERIVED FROM THERMOSTABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          United States of America
                                                                                                                                                                                                                                                                   UNITED STATES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32,837
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                                                                                                                                                                                                                                                                   OF AMERICA
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Pred. No. 2.4e+02;
Prematches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Version #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 834;
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RESULT 13
US-08-384-490-31
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US-08-384-490-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                           TELEFAX: (510) 814-297
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 834 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 834 amino acids
               MOLECULE TYPE:
                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Sias, Stacey R.
REGISTRATION NUMBER: 32,630
                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384,490
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gelfand, David H.
APPLICANT: Lawyer, Frances C.
APPLICANT: Stoffel, Susanne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: FO TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38.1%;
Local Similarity 61.5%;
nes 8; Conservativo
                            STRANDEDNESS:
TOPOLOGY: lir
                                                                TYPE:
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 FVVFDAKAPSFRH 76
                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                              amino acid
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5618711
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: U.S.A.
                                                                          834 amino acids
                                linear
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                                                                                                                                               (510) 814-2863
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               DNA (genomic)
                                           single
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                                                                                                                              814-2977
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                                                                                                               31:
                                                                                                                                                                               8887
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Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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US-08-459-383-31
Sequence 31, Application US/08459383
Patent No. 5741690
GENERAL INFORMATION:
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                                                                                                                                                                                                                                            ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-483-043-6
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 415/705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Peter G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 04-JUN-1993
APPLICATION NUMBER: US 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 220 CITY: San Francisco
STATE: California
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lyamichev, Victor I.
APPLICANT: Brow, Mary Ann D.
TITLE OF INVENTION: SYNTHESIS-DEFICIENT THERMOSTABLE DNA
TITLE OF INVENTION: POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                Local Similarity hes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/483,043 FILING DATE: 06-JUN-1995 CLASSIFICATION: 435
                                                                                                                   64 FVVFDAKAPSFRH
                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 32
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Pred. No.
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Pred. No. 2.4e+02;
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APPLICANT:

Gelfand, David H.

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CIP: 07110

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,383

FILING DATE:
APPLICATION NUMBER: US/08/384,490

FILING DATE:
APPLICATION NUMBER: US/08/148,133

FILING DATE:
APPLICATION NUMBER: US/08/148,133

FILING DATE:
APPLICATION NUMBER: 32,630

REFERENCE/DOCKET NUMBER: 8887

TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2863

TELEFAX: (510) 814-2863
Search completed: March 27, 2003, 10:07:34 Job time: 5.63415 secs
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CORRESPONDENCE ADDRESS:
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APPLICANT: Stoffel, Susanne
TITLE OF INVENTION: Recombinant Expression Vectors and
TITLE OF INVENTION: Purification Methods for Thermus Thermophilus DNA
TITLE OF INVENTION: Polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 340 K
CITY: Nutley
STATE: New Je
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New Jersey COUNTRY: U.S.A. ZIP: 07110
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                       Cucumber raffinose
Cucumber raffinose
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Amino acid sequenc
Soybean raffinose
Broad bean raffino
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Cucumber raffinose
Amino acid sequenc
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38.1	38.1	38.1	38.1	38.1	38.1	38.1	38.1	38.1	38.1	•	9	9	9	0			0.	0	1	1	1.	1.	1.	_	1.	2	4	44.3	4	٠	٠	'n		
283	232	146	145	144	129	78	52	52	48	823	212	212	212	382	382	257	22	841	447	441	313	86	428	421	112	763	783	777	295	253	175	770	783	758
23	22	22	20	20	22	22	22	22	22	22	20	20	20	22	22	17	20	21	21	20	22	23	22	22	18	21	23	20	21	21	21	21	20	21
20	225	73	AAY48481	AAY59807	AAM00853	AAU47171	ABG01021	ABG01020	AAO10988	ABG19520	AAW82685	AAW82678	AAW82677	AAB76725	AAG90340	AAR94460	AAY13176	AAY70981	AAG15496	AAY40501	AAB50675	ABP31035	ABB60476	ABB63148	AAW08433	AAY70977	ABB93664	AAY32074	AAG16863	AAG16864	AAG16865	AAY70976	3207	AAY70978
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## ALIGNMENTS

RESULT 1 AAW53568

AAW53568 standard; peptide; 19

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Cucumber raffinose synthase residues 61 to 79

06-JUL-1998 (first entry)

AAW53568;

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Cucumis sativus
                                                                                                                                              Cucumber; raffinose synthase; sucrose; galactinol
           Example 2; Page 17; 26pp;
                        Raffinose synthase gene - transformed plant
                                            WPI; 1998-264858/24.
                                                                       26-JUL-1996;
26-APR-1996;
                                                                                           28-APR-1997;
                                                                                                        07-APR-1998
                                                                                                                    JP10084973-A.
                                                         (AJIN ) AJINOMOTO KK
                                                                      96JP-0198079.
96JP-0107682.
                                                                                          97JP-0111124
           Japanese
                               useful for preparation
                                of.
                                raffinose
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The present sequence is a cucumber raffinose synthase fragment.

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AAW53570
ID AAW5
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AC AAW5
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Matches 19
                                                                                                             Best Loc
Matches
                                                                                                                             Query Match
                                                                                                                                                                   The present invention describes a raffinose synthase, having an activity of forming raffinose from sucrose and galactinol. The raffinose synthase gene can be used for expression in a plant for the production of raffinose. The raffinose synthase can give raffinose from sucrose and galactinol efficiently. The present sequence represents a raffinose control of from sucrose and galactinol efficiently.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Raffinose synthase forms raffinose from sucrose and galactinol, he an optimum pH of 6 to 8 and working temperature of 35 to 40 degree C, has a molecular weight of 75 to 95 kDa by gel filtration or 90 to 100 kDa by PAGE and SDS-PAGE under reductive conditions and is inhibited by iodoacetamide, N-ethylmaleimide and myoinositol.
   06-JUL-1998
                   AAW53570;
                                   AAW53570
                                                                                                                                              Sequence
                                                                                                                                                              synthase
                                                                                                                                                                                                                                       sucrose and
                                                                                                                                                                                                                                      New raffinose synthase gene - sucrose and galactinol
                                                                                                                                                                                                                                                                WPI; 1999-340516/29
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les 19; Conserv
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                                                                                            PVSVGCFVGFDASEPDSRH 19
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                                                                                                                                                                                                                     2; Page 21; 37pp; Japanese.
                                                                                                                                                            peptide from
                                  standard;
                                                                                                                                              19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  (first
 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AΑ;
                                                                                                                                                                                                                                                                                                97JP-0292969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide;
                                   Protein;
                                                                                                                                                                                                                                                                                                                                                                                 sucrose; galactinol
                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100
                                                                                                                                                              cucumber.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .0%;
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                                    784
                                                                                                             0;
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                                                                                                            Score 105; DB 20;
Pred. No. 2.6e-10;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 105; DB 19;
Pred. No. 2.6e-10;
; Mismatches 0;
                                                                                                                                                                                                                                               for
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
                                   AA
                                                                                                                                                                                                                                              production of raffinose from
                                                                                                                                                                                                                                                                                                                                                                                                 ID NO:2.
                                                                                                             Indels
                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                             19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           degrees
                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                      an activity
                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              has
                                                                                                                                                                                              synthase
                                                                                                             0;
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                                                                                                                                                                                                                     RESULT 4
AAY17417
ID AAY1
   В
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                                                                                                                                                                                                                                                                                                                                sucrose and galactinol
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cucumis
                                                                                                                                                                                                                                                                61
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Query Match
Best Local S
Matches 19
                                  WPI; 1999-340516/29
N-PSDB; AAX61238.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is cucumber raffinose synthase, which forms raffinose from sucrose and galactinol, has an optimum pH of 6 to 8 and working temperature of 35 to 40 degrees C, has a molecular weight of 75 to 95 Kpa by gel filtration or 90 to 100 by PAGE and SDS-PAGE under reductive conditions and is inhibited
                                                                                                                                                                                                                                 JP11123080-A.
                                                                                                                                                                                                                                                                  Cucumis sativus
                                                                                                                                                                                                                                                                                                                                       Cucumber raffinose
                                                                                                                                                                                                                                                                                                                                                                                                          AAY17417;
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY17417 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Pages 17-20; 26pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Raffinose synthase gene - useful for preparation transformed plant % \left( 1\right) =\left\{ 1\right\} =\left\{ 1\right\} 
 New raffinose synthase
                                                                                                                                                            24-OCT-1997;
                                                                                                                                                                                                                                                                                                  Raffinose synthase;
                                                                                                                                                                                                                                                                                                                                                                         29-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAV22250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JUL-1996;
26-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cucumber; raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cucumber raffinose synthase
                                                                                       (AJIN ) AJINOMOTO KK
                                                                                                                                                                                              11-MAY-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AJIN ) AJINOMOTO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JP10084973-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lodoacetamide, N-ethylmaleimide and myoinositol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 PVSVGCFVGFDASEPDSRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVSVGCFVGFDASEPDSRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1998-264858/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sativus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       784 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                        (first
                                                                                                                           97JP-0292969
                                                                                                                                                              97JP-0292969
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                                                                                                                                                                                                                                                                                                                                     synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                    sucrose;
                                                                                                                                                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synthase; sucrose; galactinol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
gene -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19
                                                                                                                                                                                                                                                                                                                                                                                                                                             784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                    galactinol.
   for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 105; DB 19;
Pred. No. 1.2e-08;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                             AΑ
 production of raffinose from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0f
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    784;
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bited by
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Best Local
                                                                                                  Matches
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                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a raffinose synthase, having an activity of forming raffinose from sucrose and galactinol. The raffinose synthase gene can be used for expression in a plant for the production of raffinose. The raffinose synthase can give raffinose from sucrose and galactinol efficiently. The present sequence represents raffinose
                                                                                                                                                                                                                                                                             The present invention relates to a mutant protein of raffinose synthase in which at least one aromatic amino acid present at the position of about 1-7 amino acids from the N-terminus is deleted or replaced. The mutant protein can be used for reducing the raffinose oligosaccharide content in a plant body. The present protein from soybean, was used in
                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-JUL-2000; 2000JP-0200571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JP2001078783-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plant; soybean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mutant; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soybean protein:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB98659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB98659 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         synthase from cucumber.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel mutant protein of raffinose synthase is useful for reducing raffinose oligosaccharide content in a plant body -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAH27438.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-313373/33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SUMO ) SUMITOMO CHEM
68
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                                              4 VGCFVGFDASEPDSRH 19
                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 PVSVGCFVGFDASEPDSRH 19
                                                                                                                                                                                                                                                       present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PVSVGCFVGFDASEPDSRH 79
                                                                                                  l Similarity
13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        784 AA;
                                                                                                                                                                                                        780 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 18-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99JP-0196036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          raffinose synthase; raffinose oligosaccharide reduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                           67.6%;
81.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          30pp;
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                                                                                                0
                                                                                                                      Score 71;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 105; DB 20;
Pred. No. 1.2e-08;
; Mismatches 0;
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                                                                                                  Mismatches
                                                                                                                           DB 22;
0.0044;
                                                                                                                                              Length 780;
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                                                                                                Gaps
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RESULT

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RESULT 7
AAY30143
ID AAY3
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ID AAW5
В
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Best Local S
Matches 13
                                                                                                                                                                                                                                                                                                                                   This sequence represents the soybean raffinose synthetase of the invention. The raffinose synthetase is capable of producing raffinose by combining a D-galactosyl group through an alpha (1-6) bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule. The DNA can be used to modify metabolism of a host organism by introducing into the host organism or its cell so that the content of the raffinose family oligosaccharides are useful as food additives with beneficial effects on the gastrointestinal flora.
                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 31-34; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid molecule encoding plant raffinose synthetase capable of producing raffinose, used as food additives with beneficial effects on gastrointestinal flora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-324670/29.
N-PSDB; AAV40801.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Raffinose synthetase; metabolism modification; gastrointestinal flora; soybean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Soybean raffinose synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW57887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW57887 standard; Protein; 781 AA
                     JP11215984-A.
                                           Glycine max.
                                                                Raffinose synthase;
                                                                                       Amino acid sequence of a raffinose synthase protein.
                                                                                                                                                            AAY30143 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-DEC-1997;
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                                                                                                               26-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SUMO ) SUMITOMO CHEM CO LTD
                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                 4 VGCFVGFDASEPDSRH 19
                                                                                                                                                                                                                  VGCFVGFHADEPRSRH
                                                                                                                                                                                                                                                                 l Similarity
13; Conserv
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                                                                                                                                                                                                                                                                                                                781 AA;
                                                                                                                                                                                                                                                                  Conservative
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                                                                                                              (first entry)
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                                                                                                                                                           Protein;
                                                                 plant;
                                                                                                                                                                                                                                                                            67.6%;
81.2%;
                                                                                                                                                                                                                     83
                                                                  sucrose;
                                                                                                                                                            781
                                                                                                                                                                                                                                                                           Score 71;
Pred. No.
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                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                           DB 19;
0.0044;
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RESULT 8
AAB49400
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DT 07-M
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Best Local S
Matches 13
 Query Match
                                    Sequence
                                                                                                                                         Example 6; Page 24-27;
                                                                                                                                                                                                                                                                                                                                                         30-APR-1999;
01-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Soybean raffinose synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB49400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB49400 standard; Protein; 781 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a raffinose synthase protein. The sequence is isolated from plant material. The protein forms raffinose by complexing alpha(1 to 6)- D-galactosyl hydroxyl group of the 6C of D-glucose residue in sucrose molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; Page 25-27; 40pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAZ10002
                                                                                                                                                                                             New soybean plant promoters useful for generating transgenic plants
                                                                                                                                                                                                                                                                                                                                                                                                            27-APR-2000; 2000EP-0108962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New raffinose synthase gene - is prepared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-511112/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-DEC-1997;
                                                                                                                                                                                                                                                                                   Ishige F,
                                                                                                                                                                                                                                                                                                                      (SUMO ) SUMITOMO CHEM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-NOV-1997;
18-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SUMO ) SUMITOMO CHEM CO LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 VGCFVGFDASEPDSRH 19
                                                                                     present invention provides novel plant production of transgenic plants which \boldsymbol{\varepsilon}
                                                                                                                                                                               desired
                                                                                                                                                                                                                                                  2001-104537/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VGCFVGFHADEPRSRH 83
                                                                                                                                                                                                                                  AAC89523
                                                                                                                                                                                                                                                                                   Watanabe
                                      781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       781 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                           properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first
                                                                                                                                                                                                                                                                                                                                                         99JP-0124527.
99JP-0247211.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96JP-0338673.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97JP-0342899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transgenic plant; desired property.
                                                                                                                                                                                                                                                                                   Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.6%;
81.2%;
   67.6%;
                                                                                                                                         36pp; English
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Pred. No.
   Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
   71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 20;
0.0044;
   DΒ
                                                                                     express genes
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 22;
 Length 781;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plant material
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                         which can
nes with de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                       an be used
desired
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                                                                                                         in
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RESULT 10
AAY30142
ID AAY30
XX
AC AAY30
AC AAY30
XX
DT 26-OC
XX
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                                                    AAY30142;
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RESULT 9
AAW57886
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Matches
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                                                                                                                                                                                                                                                                    This sequence represents the broad bean raffinose synthetase of the invention. The raffinose synthetase is capable of producing raffinose by combining a D-galactosyl group through an alpha (1-6) bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule. The DNA can be used to modify metabolism of a host organism by introducing into the host organism or its cell so that the content of the raffinose family oligosaccharides are useful as food additives with beneficial effects on the gastrointestinal flora.
AAY30142 standard;
                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 26-29; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid molecule encoding plant raffinose synthetase capable of producing raffinose, used as food additives with beneficial effects on gastrointestinal flora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oeda K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW57886 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAV40800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-324670/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP849359-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vicia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gastrointestinal flora; broad bean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Raffinose synthetase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Broad bean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW57886;
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                                                                                          87
                                                                                                                                                                Local Similarity
les 10; Conserv
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                                                                                                                            GCFVGFDASEPDSRH 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGCFVGFHADEPRSRH 83
                                                                                        GCFVGFNSTEPKSHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          faba.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMITOMO CHEM CO LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wantanabe E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               raffinose synthetase
                                                                                                                                                                                                                                     799 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96JP-0338673
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 Protein;
                                                                                                                                                                                   60.0%;
66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             metabolism modification; food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            799
   799 AA
                                                                                                                                                                                 Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 0.0044;
0; Mismatches
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                                                                                                                                                                  Mismatches
                                                                                                                                                                                   63;
No.
                                                                                                                                                                                 DB 19;
0.092;
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                                                                                                                                                                                                   Length 799;
                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               additive;
                                                                                                                                                                0;
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                                                                                                                                                                Gaps
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                                                                                                                                                                0;
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(first entry)

Amino

acid

sequence

of.

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raffinose synthase protein

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RESULT 11
AAY70978
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                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a raffinose synthase protein. The sequence is isolated from plant material of broad beans. The protein forms raffinose by complexing alpha(1 to 6)- D-galactosyl hydroxyl group of the 6C of D-glucose residue in sucrose molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New
Nucleic acids and encoded proteins involved in the biosynthesis raffinose, useful for producing soybean seeds with a reduced raf content and therefore improved nutritional quality -
                                                                                                      23-OCT-1998;
                                                                                                                        22-OCT-1999;
                                                                                                                                          04-MAY-2000
                                                                                                                                                            WO200024915-A2
                                                                                                                                                                              Glycine max.
                                                                                                                                                                                              Soybean; raffinose synthase; clone sfll.pkl25.d4; nutrition
                                                                                                                                                                                                                         Soybean raffinose synthase
                                                                                                                                                                                                                                             09-AUG-2000
                                                                                                                                                                                                                                                                                 AAY70978 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; Page 19-21; 40pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-511112/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-NOV-1997;
18-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vicia faba.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Raffinose synthase;
                                                                                    (DUPO ) DU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SUMO ) SUMITOMO CHEM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-AUG-1999
                                                                                                                                                                                                                                                                                                                              87
                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                              5 GCFVGFDASEPDSRH 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     raffinose synthase gene - is prepared
                                     2000-350754/30.
DB; AAD00335.
                                                                                                                                                                                                                                                                                                                              GCFVGFNSTEPKSHH 101
                                                                                                                                                                                                                                                                                                                                                                  10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ10001
                                                                Hitz
                                                                                   PONT DE NEMOURS &
                                                                                                                                                                                                                                                                                                                                                                                                       799 AA;
                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97JP-0329006.
96JP-0338673.
                                                                                                      98US-0105451
                                                                                                                        99WO-US24923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plant;
                                                                                                                                                                                                                                                                                                                                                                          60.0%;
                                                                                                                                                                                               nutritional;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            broad
                                                                                                                                                                                                                          from clone sfll.pk125.d4
                                                                                                                                                                                                                                                                                 758 AA
                                                                                                                                                                                                                                                                                                                                                                 Score 63; DB Pred. No. 0.09
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  ω
••
                                                                                    ဗ
                                                                                                                                                                                                         raffinose saccharide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bean; sucrose;
                                                                                                                                                                                               soy protein
                                                                                                                                                                                                                                                                                                                                                                                    ВB
                                                                                                                                                                                                                                                                                                                                                                            .092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from a
                                                                                                                                                                                                                                                                                                                                                                                    20;
                                                                                                                                                                                                                                                                                                                                                                  2,
                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plant
                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                    799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       material
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           raffinose
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RESULT 12
AAY32073
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                     30-APR-1998;
30-APR-1998;
04-DEC-1998;
10-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is a raffinose synthase from clone sfl1.pkl25.d4 isolated from a soybean immature flower cDNA library sfl1. Raffinose synthase is involved in the blosynthasis of raffinose and higher homologues in the raffinose saccharide family from sucrose. The present sequence is useful for reducing the raffinose saccharide content of soybean seeds which improves the nutritional quality of the soy protein products derived from them.
          This sequence represents sugarbeet raffinose synthase, a protein that can bind a D-galactosyl group through an alpha(1-6) bond to thydroxy group attached to the carbon atom at the 6-position of the D-glucose residue in a sucrose molecule to form raffinose. cDNA (see AAZ20208) encoding the enzyme was isolated from sugarbeet containing leaf cDNA by PCR. Probes or primers generated from plant raffinose synthase genes (see AAZ20207-10) may be used to obtain
                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Raffinose synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sugarbeet raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY32073 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                         raffinose
                                                                                                                                  New sense
                                                                                                                                                        N-PSDB; AAZ20208
                                                                                                                                                                                           Watanabe
                                                                                                                                                                                                                                                                                            27-APR-1999;
                                                                                                                                                                                                                                                                                                                  03-NOV-1999
                                                                                                                                                                                                                                                                                                                                       EP953643-A2
                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                             Beta vulgaris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY32073;
                                                                                                                                                                                                               (SUMO ) SUMITOMO CHEM CO LTD
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                                                                                                                                                                     1999-593144/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVGCFVGFDASEPDSRH
 raffinose synthase genes
                                                                                                    25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Page 47-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
10; Conser
                                                                                                                                                                                          'n
                                                                                                                      and antisense genes, in food plants -
                                                                                                 Page 22-24; 55pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         758 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                           Oeda K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                    98JP-0120550.
98JP-0120551.
98JP-0345590.
98JP-0351246.
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                                                                                                                                                                                                                                                                                                                                                             /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  sugarbeet;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        synthase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58pp;
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                                                                                                                                                                                                                                                                                                                                                            "encoded by CCR"
                                                                                                                                                                                                                                                                                                                                                                                  "encoded
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           783
                                                                                                 English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 62; [
Pred. No. 0.
 γģ
                                                                                                                                   useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                  transgenic plant
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labeled detection
                                                                                                                                                                                                                                                                                                                                                                                  CCM.
                                                                                                                                   for altering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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 amplification
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RESULT 13
AAY70976
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                 The present sequence is a raffinose synthase from clone rls24.pk0017.g10 isolated from a rice infected leaf cDNA library rls24. Raffinose synthase is involved in the biosynthesis of raffinose and higher homologues in the raffinose saccharide family from sucrose. The present sequence is useful for reducing the raffinose saccharide content of soybean seeds which improves the nutritional quality of the soy protein products derived from them.
                                                                                                                      Claim 2; Page 40-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (claimed). These genes may be used to control the levels of raffinose produced in plants. Antisense genes can be used to knock out existing gene activity, and sense genes to increase the level of gene activity. The resulting transgenic plants may be used as a food source to alter the growing conditions for gut enterobacteria, providing general health advantages.
Sequence
                                                                                                                                           Nucleic acids and encoded proteins involved in the biosynthesis of raffinose, useful for producing soybean seeds with a reduced raffinose content and therefore improved nutritional quality -
                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                   Allen
                                                                                                                                                                                                                                                        (DUPO)
                                                                                                                                                                                                                                                                                 23-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                  04-MAY-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rice;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY70976;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60
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                                                                                                                                                                                              2000-350754/30.
DB; AAD00333.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLFVGFDAPEPKARH 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     raffinose synthase; raffinose saccharide; r1s24.pk0017.g10; nutritional; soy proteir
                                                                                                                                                                                                                                                          DU
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770
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AA,
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                                                                                                                                                                                                                                                                                 98US-0105451.
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                                                                                                                                                                                                                                                                                                                                                                                            /label= Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Encoded by a
                                                                                                                                                                                                                                                        NEMOURS & CO E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                    58pp; English.
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73.3%;
                                                                                                                                                                                                                                                                                                                                                                               770
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
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                                             the raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
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Query Match

45

. 28;

Score 47.5;

DВ

21;

Length

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RESULT 14
AAG16865
ID AAG16665
XX AAG16
XX AAG16
XX Prote
KW Prote
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25 MAY 1999
27 MAY 1999
28 MAY 1999
01 JUN 1999
03 JUN 1999
04 JUN 1999
07 JUN 1999
07 JUN 1999
10 JUN 1999
11 JUN 1999
11 JUN 1999
11 JUN 1999
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30-APR 1999
04-MAY 1999
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06-MAY 1999
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07-MAY 1999
11-MAY 1999
14-MAY 1999
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21-MAY-1999;
24-MAY-1999;
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29-MAR-1999;
01-APR-1999;
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09-MAR-1999;
23-MAR-1999;
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14-MAY-1999;
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21-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hybridisation assay; genetic mapping; gene expression control;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein identification; signal transduction pathway; metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG16865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG16865 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           termination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39 PVD-GVFLGGDFAEPASRH 56
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99US-0136782.
99US-0137228.
99US-0137528.
99US-0137502.
99US-0137724.
99US-0138094.
99US-0138840.
99US-0138847.
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990S-0134218.
990S-0134219.
990S-0134221.
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990S-0134370.
990S-0134768.
990S-0134941.
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99US-0127862.
99US-0127862.
99US-012834.
99US-0128047.
99US-0130077.
99US-0130449.
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99US-0136392
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99US-0135353
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99US-0132863
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Best Local S
Matches 9
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113-AUG-1999
114-AUG-1999
116-AUG-1999
117-AUG-1999
117-A
                            h 44.8
Similarity 64.3
9; Conservative
                                                                                  9908-0148341
9908-0148684
9908-014958
9908-0149902
9908-0149902
9908-0150866
9908-0150866
9908-0151086
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9908-0151373
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   18
                                          Score 47; DB Pred. No. 8; 2; Mismatches
                                                         ВВ
                                                         21;
                                                       Length
                               Indels
                                                          175;
                              0
                              Gaps
                              0
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16-JUN-1999
17-JUN-1999
18-JUN-1999
18-JUN

99US-0139452.
99US-0139453.
99US-0139455.
99US-0139455.
99US-0139456.
99US-0139466.
99US-0139466.
99US-0139462.
99US-0139463.
99US-0139763.
99US-0140354.
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99US-014085.
99US-014334.
99US-014334.
99US-014335.
99US-014433.
99US-014591.
99US-014591.
99US-014591.
99US-014591.
99US-014591.
99US-014591.
99US-0147303.

GCFVGFDASEPDSR

В 90 GEFLGFDENEPTSR 103

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RESULT 15
AAG16864
ID AAG16
XX AAG16
XX AAG16
XX AAG16
XX AAG16
XX Prote
XX 25-FE
PR 05-MB
PR 05-MB
PR 25-MB
PR 16-AE
PR 23-AE
PR 16-AE
PR
25-FEB-1999
05-MAR-1999
09-MAR-1999
23-MAR-1999
24-MAR-1999
16-APR-1999
16-APR-1999
16-APR-1999
23-APR-1999
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23-APR-1999
23-APR-1999
23-APR-1999
24-MAY-1999
30-APR-1999
31-MAY-1999
31-MAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
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990S-0121825
990S-0123180
990S-0123548
990S-0125788
990S-0126264
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990S-0128214
990S-0130449
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990S-0134218
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## ALIGNMENTS

3-phosphoserine phosphatase [imported] - Arabidopsis thaliana
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C.Accession: B86320
R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A.; Althors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.;Reference and analysis of chromosome 1 of the plant Arabidopsis.
A.;Reference number: A86141; MUID:21016719; PMID:11130712 C;Accession: AF3233
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
B;Authbors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam ster, E.W. conserved hypothetical protein Atu6048 [imported] - Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002 RESULT B86320 A; Genome: plasmid C; Superfamily: Lactococcus lactis hypothetical protein PL08712.1C;Genetics: A;Gene: Atu6048 A;Reference number: AB2577; PMID:11743193
A;Accession: AF3233
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-836 <KUR>
A;Residues: 1-836 <KUR>
A;Cross-references: GB:AE008690; PIDN:AAL46284.1; PID:917744066; GSPDB:GN00189 A; Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A; Reference number: AB2577; PMID:11743193В δÃ A; Experimental source: strain C58 (Dupont) Query Match Best Local Matches 687 NLGAYLGFDAERPEAVH 703 Local Similarity es 7; Conserv 3 SVGCFVGFDASEPDSRH 19 Conservative 46.7%; Pred. No. Score 49; Mismatches σ DB 2; 4; Indels Length 836; 0 Gaps 0: (strain

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-295 <S7
A;Cross-references: C
C;Genetics:
A;Map position: 1
                                               A; Map position:
C; Superfamily: 1
                                                                                                                                                                                   A; Reference number: A97359; A; Accession: A97544
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A.; Liu, F.; Wollam, C.; Al
Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                               C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
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A;Pathway: serine biosynthesis (plastidic pathway)
C;Keywords: chloroplast; phosphoric monoester hydrolas
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C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000
C;Accession: T51362
                                                                                                                  A; Residues: 1-336 < KUR>
A; Cross-references: GB:
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J. Biol. Chem. 274, 11007-11012,
A;Title: Plastidic pathway of ser
A;Reference number: Z25385
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N;Alternate names: 3-phosphoserine phosphatase
C;Species: Arabidopsis thaliana (mouse-ear cress)
                                                                                                                                                   A; Molecule type: DNA
                                                                                                                                                                  A; Status: preliminary
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A; Residues: 1-295 <HOC>
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                                                                                                                                                                                                                                                 G.; Gattung, S.; Miller, N.; Blanchard, M.; Quro C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas,
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 44.8%;
47.1%;
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64.3%;
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                                                                                                                PIDN:AAK87306.1;
 Score
Pred.
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Pred. No.
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 47;
No.
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4.8;
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DB;
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               Length 336
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                                                                                                                GSPDB:GN00169
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Markelz, B.
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GTP-binding protein | C;Species: Brucella n C;Species: 01-Feb-2002 t C;Date: 01-Feb-2002 t C;Accession: AH3445
                             Ωy
                                                                                                                             C; Superfamily: Mycobacterium leprae probable GTP-binding protein;
                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-483 < KUR>
                                                                                                                                                                                                                                                                            R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucell A;Reference number: AD3252; PMID:11756688
A;Accession: AH3445
DЬ
                                                                                                                                                A; Map
                                                                                                                                                                A; Gene: BMEI1550
                                                                                                                                                                                                A; Experimental source: strain 16M
                                                                                                                                                                                                              A;Cross-references: GB:AE008917; PIDN:AAL52731.1; PID:g17983561; GSPDB:GN00190
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, erage, G.; Gillet, W.; Grant, C.; Guenthner,
                                                                                                                                                                                                                                                              A; Status: preliminary
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C; Superfamily: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-336 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Authors: Yoo, H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conserved hypothetical protein Atu1515 [imported] -
C;Species: Agrobacterium tumefaciens
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Best Local
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8; Conserv
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Haemophilus influenzae
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                                                                                                                                                                                                                                                                                                                                                                                                                 [imported] - Brucella melitensis (strain
melitensis
                                                                                                                                                                                                                                                                                                                                                                                                #sequence_revision 01-Feb-2002
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47.18;
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                                                                               43.8%;
47.1%;
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Pred.
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                                                                                            Score 46;
                                                               Mismatches
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12;
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D.; Let
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C;Accession: A43741
R;Baldarelli, R.M.; Mahoney, P.A.; Salas, F.; Gustavson, E.;
Dev. Blol. 125, 85-95, 1988
A;Title: Transcripts of the Drosophila blastoderm-specific lc
A;Reference number: A43741; MUID:88055884; PMID:3334721
A;Accession: A43741
                                                                                                                                                                                                                        RESULT 9
A43741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Smith, D.R.; Robison, n. submitted to the EMBL Data Library, submitted to the woobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Agaricus bisporus (cultivated mushroom)
C;Date: 06-Dec-1996 #sequence_revision 07-Feb-1997 #text_change 21-Jul-2000
C;Accession: $68584; $66586; $58942
R;de Groot, P.W.J.; Schaap, P.J.; Sonnenberg, A.S.M.; Visser, J.; van Griensven, L.J.L.I
J. Mol. Biol. 257, 1008-1018, 1996
A;Tittle: The Agaricus bisporus hypA gene encodes a hydrophobin and specifically accumula A;Reference number: $68584 MUID:96192085; PMID:8632464
A;Recession: $68584
A;Status: nucleic acid sequence not shown
                                                                                                                                                   terminus protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 04-Mar-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-301 <SMI>
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A; Accession: S73023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein L518_F3_81 - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
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A; Residues: 1-112 <DEW>
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A; Residues: 1-112 <DEG>
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preliminary
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Similarity 46.28;
6; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                             41.9%;
57.1%;
                                          Drosophila blastoderm-specific locus, MUID:88055884; PMID:3334721
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Pred. No.
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ced. No. 15;
Mismatches
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A; Molecule type: mRNA
A; Residues: 1-650 <HOR>
A; Residues: 1-650 <HOR>
A; Cross-references: GB: M91599; NID: g204137; PIDN: AAA41157.1;
R; Lai, C.; Lemke, G.
Neuron 6, 691-704, 1991
Neuron 6, 691-704, 1991
A; Title: An extended family of protein-tyrosine kinase genes
A; Reference number: PT0183; MUID: 91222580; PMID: 2025425
A; Accession: PT0191
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C;Genetics:
A;Gene: FlyBase:term
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C;Superfamily: Drosophila terminus prot
C;Keywords: DNA binding
                       C; Function:
                                        A;Gene:
                                                             C; Genetics:
                                                                                 A; Experimental source:
                                                                                                    A; Molecule type: mRNA
A; Residues: 465-518 <LAI>
                                                                                                                                                                                                                                                                                                      A;Title: Cloning, expression and tissue distribution of A;Reference number: JC1450; MUID:93013049; PMID:1398143 A;Accession: JC1450
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R;Horlick, R.A.; Stack, S.L
Gene 120, 291-295, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                              C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 01-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                 fibroblast growth factor receptor 4 - rat
N;Contains: protein-tyrosine kinase (EC 2
C;Species: Rattus norvegicus (Norway rat)
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A; Note: T22P11.70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-498 <BEV>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the Protein Sequence Database, A; Reference number: 224490 A; Accession: T48269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein T22P11.70 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Decies: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 19-May-2000 C;Accession: T48269
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A; Description: receptor mediating effects of fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source:
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nes 7; Conserv
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                                        FGFR4; tyro-9
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70.08;
                                                                                                                                                                of protein-tyrosine kinase genes MUID:91222560; PMID:2025425
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Pred. No.
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l; Mismatches
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ced. No. 22;
Mismatches
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April 2000
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziall, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Tille: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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F:110-181/Domain: immunoglobulin homology <IM2>
F:218-238/Domain: intracellular *status predicted <INM>
F:339-650/Domain: intracellular *status predicted <INT>
F:313-598/Domain: protein kinase homology <KIN>
F:313-598/Domain: protein kinase ATP-binding motif
F:321-329/Region: protein kinase ATP-binding motif
F:104,136,157,168/Binding site: carbohydrate (Asn) (covalent) *status predicted
F:465,478/Binding site: magnesium (Asn, Asp) *status predicted
F:465,478/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002 C;Accession: F86185
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A;Molecule type: DNA
A;Residues: 1-313 <MIL>
A;Cross-references: EMBL:AF067937; PIDN:AAC19217.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Miller, N.; Kramer, J.; Smith, A. submitted to the EMBL Data Library, May 1998 A;Description: The sequence of C. elegans cos A;Reference number: Z21299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein F22F7.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change C;Accession: T33185
A; Molecule
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A; Introns: 18/2; 82/3; 117/1; 210/2; 241/3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A; Accession: T33185
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Best Local
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9; Conservery
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50.0%;
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Pred. No.
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3; Mismatches
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A; Molecule type: protein A; Residues: 1-464 < TAK>
                                                                             Biochim. Biophys. Acta 1252, 185-188, 1995
A; Title: Amino-acid sequence of rat liver kynureninase.
A; Reference number: S59898; MUID:96049498; PMID:7578221
                                                                                                                                            R; Takeuchi, F.; Tsubouchi, R.; Yoshino,
                                                                                                                                                             C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Jul-1996 #sequence_revision 13
C;Accession: S59898
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Best Local Similarity
Thes 8; Conserve
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A;Molecule type: DNA
A;Residues: 1-447 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: F84733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Mierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-441 <STO>
A;Cross-references: GB:AE005172; NID:g2388583; PIDN:AAB71464.1; GSPDB:GN00141
C;Genetics:
                                    A; Status: preliminary
                                                          A; Accession: S59898
                                                                                                                                                                                                                                kynureninase (EC 3.7.1.3) - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position:
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C;Superfamily: Escherichia coli probable zinc proteinase yaeL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: T26B15.4; At2g32480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE002093; NID:g3298536; PIDN:AAC25930.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:AC004681; NID:g3298532; PID:g3298536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-447 < ROU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
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C; Keywords: hydrolase

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PORL BOVIN
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ALBU_CHICK
PEXB_DICA
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p49072 agaricus h
p11455 drosophila
p70712 rattus nor
Q18026 caenorhabe
Q8y964 anabaena s
Q9fmb0 arabidopsi
Q01886 cochliobol
p36827 human papi
p45879 bos taurus
Q9ft15 oryctolagy
Q160932 mus muscul
Q000869 paramecium
Q10719 homo sapit
p19121 gallus gal
Q00925 pichia ang
p19121 gallus gal
Q00928 thermus ca
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Q00927 pichia ang
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p19120 callus ang
p19250 thomo sapit
Q57896 methanocom
Q57896 oguine he
Q16797 drosophili
Q99q18 clostridi
Q99q18 caenorhab
p14330 caenorhab
p33449 bacillus
p04413 herpes sii
p53134 saccharom
p18269 trypanoson
p46883 escherich
p17468 bovine ro
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o arabidopsis
6 cochliobolu
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2 mus musculu
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2 homo sapien
6 mus musculu
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9 homo sapien
1 gallus gall
5 pichia angu
0 klebsiella
           saccharomyc
trypanosoma
escherichia
                                                                                                              equine herp
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36.2	36.2	36.2	36.2	36.7	36.7	36.7	36.7	37.1	37.1	37.1	37.1
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P97521 rattus norv		O54294 salmonella									

## ALIGNMENTS

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RESULT 2
TERM_DROME
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RA Ballaw R. M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Davies M., S., Davies R.,
RA Harris M.J., Evangelista C.C., Ferriaz C., Ferriera S., Fleischmann W.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., McPherson D.
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Wilsham S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Werkulow G., Janes F., Zhong W., Zhong G., Zhoa Q., Zhong L.,
RA Zhong X., Yao Q.A.,
RA Zhong S., Yao Q.A.,
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RA Zhong S., Yao R., Rohn S., Sheng L.,
RA Zhong S., Yao Q.A.,
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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
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Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
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Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
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01-OCT-1989 (Rel. 12, Created)
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16-OCT-2001 (Rel. 40, Last ann
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Baldarelli R.M., Mahoney P.A., Salas F., Gustavson E., Boyer P.D.,
Chang M.-F., Roark M., Lengyel J.A.;
"Transcripts of the Drosophila blastoderm-specific locus, terminus,
are concentrated posteriorly and encode a potential DNA-binding
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Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Terminus protein.
TERM OR TER OR CG4216.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=7227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PINLGAFLGFDCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125:85-95(1988).
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46.2%;
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RESULT 3
KYNU_RAT
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KYNU_RAT STANDARD; PRT; 464 AA.
P70712; Q9QW90;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Kynureninase (EC 3.7.1.3) (L-kynurenine hydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
SEQUENCE
                          eur.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000822; Znf_C2H2.

PROSITE; PS50157; ZINC_FINGER_C2H2_2; UNKNOWN_1.

DNA-binding; Zinc-finger; Developmental protein.

ZN_FING 325 346 C3H-TYPE.

CONFLICT 144 144 A -> V (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                    "Isolation and expression kynureninase.";
                                                                                                                  Alberati-Giani D., Buchli R., Malherbe
Koehler C., Lahm H.-W., Cesura A.M.;
                                                                                                                                                                TISSUE=Liver, and Kidney; MEDLINE=96314506; PubMed=8706755;
                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                      Toma
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochim.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Wistar;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97324088;
                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Takeuchi F., Tsubouchi R., Yoshino M., Shibata "Amino-acid sequence of rat liver kynureninase. Biochim. Biophys. Acta 1252:185-188(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96049498; PubMed=7578221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KYNU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M19140; AAA28928.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a
                                                                                                                                                                                                                                                                                     "Cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase; FBgn0003683; term
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                     FUNCTION: CATALYZES THE CLEAVAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEVELOPMENTAL STAGE: EXPRESSED FROM THE CELLULAR BLASTODERM STON, MOST DURING GASTRULATION AND IS NO LONGER DETECTED BY THE
                                                                                                                                                                                                                                                                                                                                    s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; AE003520; AAF49257.1; -. A43741; A43741
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                                                                                                                                                                                                                                                               and recombinant expression t. 408:5-10(1997).
                                                                                                                                                                                                                                                                                                                                 Nakamura M.,
                                                                                                                                                                                                                 OF 19-117
                                                                                                                                                                                                                                                                                                              Cozzi L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              428 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                            PubMed=9180257;
                                                                                                                                                                                                                    FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                           , Tone S., Oku
Speciale C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41.98;
50.08;
ES THE CLEAVAGE OF (L-30HKYN) INTO A
                                                                                       , Cesura
ion of a
                                                                                                                                                                                                               N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A -> V (IN REF. 1).
; F545653F738AE434 CRC64;
                                                                                                                                                                                                                 AND
                                                                                                                                                                                                                                                                                                              Okuno E., Kido R., Breton J.,
C., Mostardini M., Gatti S., B
                                                                                               CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                    PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                     of
                                                                                            clone
    OF L-KYNURENINE
ANTHRANILIC (A
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                                                                                                                                          Broger C.,
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  INE (L-KYN) AND L-3-
(AA) AND 3-
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                                                                                                                                                                                                                                                                                                              Benatti L.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KYNU
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                                      Kohara Y., Shin'i T.,
                                                                                                                           SEQUENCE FROM N.A.
STRAIN-Bristol N2;
                                                                                                                                                                                              Submitted
                                                                                                                                                                                                                  Bentley
                                                                                                                                                                                                                                    STRAIN-Bristol
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Rhabditidae; Peloder
                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                          C15H9.7
                                                                                                                                                                                                                                                                                                                                                                                                            Probable kynureninase
                                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-1998 (Rel. 37,
15-DEC-1998 (Rel. 37,
15-JUN-2002 (Rel. 41,
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CATALYTIC ACTIVITY: L-3-hydroxykynurenine + H(2)0 = 3-hydroxyanthranilate + L-alanine.
COFACTOR: PYRIDOXAL PHOSPHATE.
ENZYME REGULATION: INHIBITED BY O-METHYLBENZOYLALANINE PATHWAY: INVOLVED IN THE BIOSYNTHESIS OF NAD COFACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYDROXYANTHRANILIC ACIDS (3-OHAA), RESPECTIVELY. HAS A PREFER FOR THE L-3-HYDROXY FORM. DEPIMUM ACTIVITY IS AROUND PH 9.0 F KYN AND AROUND 8.5 FOR L-3OHKYN. ALSO HAS CYSTEINE-CONJUGATE-BETA-LYASE ACTIVITY. L-kynurenine + H(2)0 = anthranilate + L-CATALYTIC ACTIVITY: L-kynurenine + H(2)0 = anthranilate + L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY: HIGH LÉVELS IN LIVER AND KIDNEY. ALSO DETECTED IN HEART, RETINA, OVARY. LUNG, TESTIS AND BRAIN. INDUCTION: INHIBITED BY THIOL REAGENTS AND HEAVY METAL IOSIMILARITY: BELONGS TO THE KYNURENINASE FAMILY. SLIGHTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed.
  alanine.
COFACTOR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: HOMODIMER. SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.
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276
18
26
118
1464 AA;
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  PYRIDOXAL
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18
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52453.
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100.0%;
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                                                                                                       Suzuki Y., Sugano S.,
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Last annotation update)
(EC 3.7.1.3) (L-kynurenine hydrolase)
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PHOSPHATE
                                                                                                                                                                                            the
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D -> N (IN REF. 1).
T -> S (IN REF. 1).
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Pred. No.
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PYRIDOXAL PHOSPHATE.
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                                          anthranilate
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RESULT 5
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Best Local
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Q8YQ64;
15-JUN-2002 (Rel. 4
15-JUN-2002 (Rel. 4
15-JUN-2002 (Rel. 4
                                                                                                                                                                                                                                                                                                                                     Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T. Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.;
"Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                           cyanobacterium Anabaena sp. strain PCC 7120.
DNA Res. 8:205-213(2001).
-i- COFACTOR: 21nc (Probable).
-i- SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Hydrolase;
BINDING 289 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U56965; AAB52668.1; -. EMBL; AF303267; AAG50225.1; -. WormPep; C15H9.7; CE06835.
                                        InterPro; IPR004387;
InterPro; IPR000130;
                                                                                     MEROPS;
                                                                                                  EMBL; AP003594; BAB75670.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=21595285; PubMed=11759840;
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                                                                    InterPro; IPR001478;
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SIMILARITY: BELONGS TO THE KYNURENINASE FAMILY. SLIGHTLY RELAT
TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.
                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO PEPTIDASE FAMILY M50B SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
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7; Conserv
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478 AA;
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alloprotease All3971 (EC
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Pred. No.
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PYRIDOXAL PHOSPHATE (BY SIMILARITY).
; E889450929EC94BD CRC64;
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                                                                                                                                            (See http://www.isb-sib.ch/announce/
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ima K., Kimura T.,
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MBL outstation -
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Pfam; PF00595; PDZ;

SM00228;

TIGR00054;

mem_zinc_metalprot;

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RESULT 6
GL19_ARATH
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RX MEDLLINE=21016721; Pubmed=11130714;
RA MIJajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,
RA Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,
RA Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,
RA Miyajima N., Sasamoto S., Kimura S., Shinpo S., Takeuchi C., Wada T.,
RA Matanabe A., Yamada M., Yasuda M., Sato S., de la Bastide M.,
RA Nakazaki N., Naruo K., Okumura S., Shinpo S., Takeuchi C., Wada T.,
RA Huang E., Splegel L., Gnoj L., O'Shaughnessy A., Preston R.,
RA Huang E., Splegel L., Gnoj L., O'Shaughnessy A., Preston R.,
RA Huang E., Splegel L., Gnoj L., O'Shaughnessy A., Preston R.,
RA Huang E., Splegel L., Gnoj L., O'Shaughnessy A., Preston R.,
RA Huang E., Splegel L., Gnoj L., O'Shaughnessy A., Preston R.,
RA Huang E., Splegel L., Gnoj L., O'Shaughnessy A., Preston R.,
RA Huang E., Splegel L., Gnoj L., O'Shaughnessy A., Preston R.,
RA Huang E., Splegel L., Gnoj L., O'Shaughnessy A., Preston R.,
RA Huang E., Splegel L., Gnoj L., O'Shaughnessy A., Preston R.,
RA Huang E., Splegel L., Gnoj L., O'Shaughnessy A., Preston R.,
RA Huang E., Splegel L., Gnoj L., O'Shaughnessy A., Preston R.,
RA Huang E., Splegel L., Gnoj L., O'Shaughnessy A., Preston R.,
RA Huang E., Splegel L., Gnoj L., O'Shaughnessy A., Preston R.,
RA Huang E., Splegel L., Gnoj L., O'Shaughnessy A., Preston R.,
RA Kirchoff K., King L., Bahret A., Miller B., Marra M.,
RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.,
RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.,
RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.,
RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.,
RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.,
RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.,
RA Kirchoff K., Toth R., Willar R., Stiekema W., Pohl T.,
RA Kirchoff K., Wadler E., Peters S.,
RA Weitzeneger T., Bothe G., Rose M., Hauf J., Berneiser S., Hempel S.,
RA Huang R., Stiekema W., Fransz P., F.;

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Matches 8
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Tabata S.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last senence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative germin-like protein subfamily 1 member 9 precursor AT5G38910 OR K15E6.14 OR K15E6_90.
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                                    MEDLINE=98290546; PubMed=9628582
                                                                        SEQUENCE FROM
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                                                                                                             408:823-826(2000).
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PS00142;
                 Kaneko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0106; PDZ; 1.
0142; ZINC_PROTEASE; 1.
protein; Hydrolase; Metalloprotease; Zinc; Transmembrane;
               T., Kotani H., Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete
17
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57.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDZ;
; 54F6AAE818AEFBEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZINC (CATALYTIC) (POTENTIAL)
POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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               Υ.,
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                   Asamizu
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                 Miyajima
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Best Local
                                                                                                                                                                                                                                            HTS1_COCCA STAN

Q01886;

Q1-FEB-1994 (Rel. 2

Q1-FEB-1994 (Rel. 2

Q1-FEB-1994 (Rel. 2

15-JUN-2002 (Rel. 4

HC-toxin synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
CARBOHYD
SEQUENCE
                                                 Scott-Craig J.S., Panaccione D.G., Pocard J.-A., Walton "The cyclic peptide synthetase catalyzing HC-toxin produfilamentous fungus Cochliobolus carbonum is encoded by a 15.7-kilobase open reading frame.";
J. Biol. Chem. 267:26044-26049(1992).
                                                                                                                                                                                                                                   HTS1
                                                                                                                    SEQUENCE FROM N.A., AND PARTIAL S
STRAIN=ATCC 90305 / SB111;
MEDLINE=93100328; PubMed=1281482;
                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota;
Pleosporales; Pleosporaceae;
                                                                                                                                                                                                                                                                                                                                _cocca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
STRAIN=ATCC 90305
MEDLINE=20138231;
                                                                                                                                                                            NCBI_TaxID=5017;
                                                                                                                                                                                                                    Cochliobolus carbonum (Bipolaris zeicola)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00325; GERMIN.
PROSITE; PS00725; GERMIN; 1.
Apoplast; Cell wall; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB009048; BAI
HSSP; P45850; 1FI2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA RES. 5:41-54(1998).

-i- FUNCTION: MAY PLAY A ROLE IN PLANT DEFENSE. HAS PROBABLY NO
COXALATE OXIDASE ACTIVITY EVEN IF THE ACTIVE SITE IS CONSERVED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structural analysis of Arabidopsis thaliana chromosome 5. IV. Sequence features of the regions of 1,456,315 bp covered by nineteen physically assigned Pl and TAC clones.";
                           FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Multigene family; Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                     122
                                                                                                                                                                                                                                                                                                                                                                                                              2 VSVG-CFVGFDASEPDSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Apoplast (By simila SIMILARITY: BELONGS TO THE GERMIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: OLIGOMER (BELIEVED HEXAMER) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                     VAVGTLFVGFVTSNPENR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF01072; Germin;
                                                                                                                                                                                                                                             1994 (Rel. 28
2002 (Rel. 41
n synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR001929; Germin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              222
                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111
113
118
119
159
32
78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BAB08648.1;
                                                                                                                                                                                                                                             28, Created)
28, Last sequence update)
41, Last annotation update)
use (EC 6.3.2.-) (HTS).
/ SB111;
PubMed=10671527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111
113
118
159
49
78
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                                                                                                                                                  PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBFAMILY 1 MEMBER 9.

MANGANESE (BY SIMILARITY).

MANGANESE (BY SIMILARITY).

MANGANESE (BY SIMILARITY).

MANGANESE (BY SIMILARITY).

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
Pred.
                                                                                                                                                                                            Cochliobolus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PUTATIVE GERMIN-LIKE SUBFAMILY 1 MEMBER 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BB925CC41A905A4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     No. 12;
                                                                                                                                                                                                                                                                                                                  5217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity)
                                                                                                                                                                                                                                                                                                                  ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Manganese; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ۲.
                                                                                                                                                                                                        Dothideomycetes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                              production
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D.;
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                                                                                                                                 RESULT
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Best Local
                                                                                                                     7_HPV32
                                            VE7_HPV32
P36827;
01-JUN-1994
01-JUN-1994
15-JUN-2002
E7 protein.
                                                                                                                                                                                                                                                                                BINDING
BINDING
BINDING
                                                                                                                                                                      4200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                   REPEAT
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000873; AMP-bind.
InterPro; IPR001242; Condensatn.
InterPro; IPR003880; Ppantne_attach.
Pfam; PF00550; AMP-binding; 4.
Pfam; PF00550; pp-binding; 4.
Pfam; PF00668; Condensation; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M98024; AAA33023.1; -. HSSP; P14687; 1AMU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol. Chem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cheng
           Human papillomavirus type 32 Viruses; dsDNA viruses, no R
                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00012; PHOSPHOPANTETHEINE; PROSITE; PS00455; AMP_BINDING; 3. PROSITE; PS50075; ACP_DOMAIN; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                      SEQUENCE
Papillomavirus
                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0154; AMPBINDING
                                                                                                                                                                                             5 GCFVGFDASEPDSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FROM L-Ala by TOXG.

COPACTOR: CONTAINS 4 COVALENTLY BOUND PHOSPHOPANTETHEINES.

PATHMAY: NON-RIBOSOMAL BIOSYNTHESIS OF HC-TOXIN.

SIMILARITY: BELONGS TO THE ATP-DEPENDENT AMP-BINDING ENZYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS 4 ACYL CARRIER DOMAINS.

CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-3 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proline and AEO (2-amino-9,10-epoxi-8-oxodecanoic acid), and epimerize L-Pro. Catalyzes the production of HC-toxin: a cyclic tetrapeptide. Activates and thioesterifies L-Pro, and epimerizes it to D-Pro; also uses D-Ala as a substrate but this is epimerize.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Non-ribosomal peptide synthetase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                     GCFVPLDPSYPHER
                                                                                                                                                                                                                    Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                Multifunctional
                                                         (Rel. 29, Created)
(Rel. 29, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Walton J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alanine racemase gene involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   275:4906-4911(2000).
                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                      3
                                                                                                                                                                                                                                                                                 803
2414
3568
4700
                                                                                                                                                                                                                                                                                                                               2452
3606
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840
2450
2450
3604
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                                                                                                                                                                                             18
                                                                                                                                                                                                                                39.0%;
                                                                                                                                                                                                                                                                     574637
                                                                                                                                                                                                                                                                                                                                                                                                                               enzyme; Phosphopantetheine; Repeat
           RNA stage;
                                                                                                                                                                                                                                                                     MW;
                                                                                                                                                                                                                                                                                                                             DOMAIN 4.

ACYL CARRIER (ACP)

ACYL CARRIER (ACP)

ACYL CARRIER (ACP)

ACYL CARRIER (ACP)
                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                 Score
Pred.
                                                                                                                                                                                                                                                                               PHOSPHOPANTECHEINE (BY SIMILARITY).
PHOSPHOPANTECHEINE (BY SIMILARITY).
PHOSPHOPANTECHEINE (BY SIMILARITY).
PHOSPHOPANTECHEINE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                           PRT;
                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                     0331D9C5400163A5
                                                                                                           104
            Papillomaviridae;
                                                                                                                                                                                                                Db -
3.6e+02;
6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       There are no restrictions on ong as its content is in no
                                                                                                           ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Usage
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                                                                                                                                                                                                                                           Length 5217;
                                                                                                                                                                                                                                                                                                                               <u> 4 ω ν 1</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cyclic peptide
                                                                                                                                                                                                                                                                      CRC64;
                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL outstation
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PACE PROPERTY OF THE PROPERTY 
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P458/7;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Voltage-dependent anion-selective channel protein 1 (VDAC-1)
Voltage-dependent anion (Brain-derived voltage-dependent anion channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000148; Papvi_E7.
Pfam; PF00527; E7; 1.
Early protein; Transcription regulation; Oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Curr. Top. Microbiol. Immunol. 186-i- FUNCTION: E7 PROTEIN HAS BOTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VDAC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POR1_BOVIN
P45879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                     Proc.
                                                                                                                                                                                                                       membranes.";
Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                             Siemen D.;
                                                                                                                                                                                                                                                                                                                                                 Dermietzel R., Hwang
Kremer M., Deutzmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria;
Bovidae; Bovinae; Bo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S36510; S36510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X74475; CAA52550.1; -.
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Curr. Top. Microbiol. Immunol. 186:13-31(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Delius H., Hofmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94265501; PubMed=8205838;
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                                                                                                                                                                                                                                                                     constitutes a large-conductance anion channel in
                                                                                                                                                                                                                                                                                                                                               Kremer M.,
                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94119914;
                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                   "Cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28
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                                                                                                                   C. Natl. Acad. Sci. U.S.A. 91:499-503(1994).

FUNCTION: FORMS A CHANNEL THROUGH THE MITOCHONDRIAL OUTER MEMBRANE AND ALSO THE PLASMA MEMBRANE. THE CHANNEL ALLOWS DIFFUSION OF SMALL HYDROPHILIC MOLECULES; IT ADOPTS AN OPEN CONFORMATION AT LOW OR ZERO MEMBRANE POTENTIALS AND A CLOSED CONFORMATION AT POTENTIALS
     TISSUE
                                                ABOVE 30-40 MV. THE OPEN STATE HAS A WEAK ANION SELECTIVITY WHEREAS THE CLOSED STATE IS CATION-SELECTIVE. SUBCELLULAR LOCATION: OUTER MEMBRANE OF MITOCHONDRIA AND PL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTIVITIES.
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     SPECIFICITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                 situ
                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=7507248;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11591 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.1%;
                                                                                                                                                                                                                                                                                                                                               T.-K., Buettner R., R., Thinnes F.P., F.
                                                                                                                                                                                                                                                                                              localization
     PREDOMINANTLY IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40; I
Pred. No. 9
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                                                                                                                                                                                                                                                                                                 brain-derived
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Fishman G.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  There are no restrictions as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
     BRAIN ASTROCYTES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 104;
                                                                                                                                                                                                                                                                       astrocytic plasma
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., Spray
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                                                     PLASMA
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RESULT 10
POR1_RABIT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                  Pfam; PF01459;
                                                                                                                                                           the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Voltage-dependent anion selective channel protein
                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mitochondrial membrane protein porin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POR1_RABIT
                                                [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                 Rae J.L
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00185; EUKARYTPORIN.
PROSITE; PS00558; EUKARYOTIC_F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X75068; CAA52962.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- DOMAIN: CONSISTS MAINLY OF MEMBRANE-SPANNING SIDED BETA-SHEETS.
-1- SIMILARITY: BELONGS TO THE EUKARYOTIC MITOCHONDRIAL PORIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 INLGCDVDFDIAGPSIR 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .asma; Porin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VSVGCFVGFDASEPDSR 18
                                                                                                                                                                                                        DOMAIN: CONSISTS MAINLY OF MEMBRANE-SPANNING SIDED BETA-SH
SIMILARITY: BELONGS TO THE EUKARYOTIC MITOCHONDRIAL PORIN
                                                                                                                                                       European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                              NITTED (DEC-1999) to the EMBL/GENBANK/DDBJ databases.
FUNCTION: FORMS A CHANNEL THROUGH THE MITTOCHONDRIAL OUTER MEMBRANE AND ALSO THE PLASMA MEMBRANE. THE CHANNEL ALLOWS DIFFUSION OF SMALL HYDROPHILIC MOLECULES; IT ADOPTS AN OPEN CONFORMATION AT LOW SMALL HYDROPHILIC MOLECULES;
                                                                                                                                                                                                                                                                  OR ZERO MEMBRANE POTENTIAL AND A CLOSED CONFORMATION AT POTENTIALS ABOVE 30-40 MV. THE OPEN STATE HAS A WEAK ANION SELECTIVITY WHEREAS THE CLOSED STATE IS CATION-SELECTIVE (BY SIMILARITY). SUBCELLULAR LOCATION: OUTER MEMBRANE OF MITOCHONDRIA AND PLASMA
                                                                                                                                                                                                                                                      MEMBRANE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
                                            AF209725; AAF22835.1; -. Pro; IPR001925; Porin_Euk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF01459; Euk_porin;
                PR00185;
                                                                                           non-profit institutions as long d and this statement is not removed. s requires a license agreement (See an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                              Zealand white; TISSUE=Corneal endothelium;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cuniculus (Rabbit)
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                               Euk_porin;
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                 EUKARYTPORIN.
EUKARYOTIC_PORIN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38.1%;
41.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leporidae; Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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27;
                                                                                                                                                  There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vertebrata; Euteleostomi;
                                                                                                                                         as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Length 282;
                                                                                                                          Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (VDAC-1) (Outer
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                                                                                                                                                                                                                                      BETA-SHEETS
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                                                                                                                                                                         outstation
                                                                                                                                                                                                                       FAMILY.
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RESULT
POR1_MC
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Best Local Similarity
Thes 7; Conserve
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MOD_RES
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _MOUSE
   MGD; MGI:106919; Vdac1
                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restitute the European Bioinformatics Institute.
                                                                                                                                                                                         -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; PL-VDAC1 (SHOWN HERE) AND MT-VDAC1; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: HIGH LEVELS OF EXPRESSION DETECTED IN HEART,
KIDNEY, BRAIN, AND SKELETAL MUSCLE. NOT EXPRESSED IN TESTIS.
-!- DOMAIN: CONSISTS MAINLY OF MEMBRANE-SPANNING SIDED BETA-SHEETS.
-!- SIMILARITY: BELONGS TO THE EUKARYOTIC MITOCHONDRIAL PORIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Voltage-dependent anion-selective channel protein 1 (VDAC-1) (mVDAC1)
(mVDAC5) (Outer mitochondrial membrane protein porin 1) (Plasmalemmal
                                           EMBL; U30840;
                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                       anion channel isoform.";
Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VDAC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q60932;
15-JUL-1999
                                                                                                   modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Buettner R., Papoutsoglou G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHARACTERIZATION, AND ALTERNATIVE SPLICING MEDLINE=20202612; PubMed=10716730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        voltage-dependent anion channel isoforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96301405; PubMed=8660977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Outer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomics 33:283-288(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Isolation, characterization, and mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sampson M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM MT-VDAC1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POR1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Evidence for secretory pathway localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 INLGCDVDFDIAGPSIR 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VSVGCFVGFDASEPDSR
                                                                                                                                                                                                                                                                                               ABOVE 30-40 MV. THE OPEN STATE HAS A WEAK ANION SELECTIVITY WHEREAS THE CLOSED STATE IS CATION-SELECTIVE.
SUBCELLULAR LOCATION: MITOCHONDRIAL VDAC1 (MT-VDAC1) IN OUT.
MEMBRANE OF MITOCHONDRIA AND PLASMALEMMAL VDAC1 (PL-VDAC1)
                                                                                                                                                                                                                                                                                                                                                            FUNCTION: FORMS A CHANNEL THROUGH THE MITOCHONDRIAL OUTER MEMBRANE AND ALSO THE PLASMA MEMBRANE. THE CHANNEL ALLOWS DIFFUSION OF SMALL HYDROPHILIC MOLECULES; IT ADOPTS AN OPEN CONFORMATION AT LOW OR ZERO MEMBRANE POTENTIAL AND A CLOSED CONFORMATION AT POTENTIALS
                                                                                                                                                                                                                                                                                      PLASMA MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OR VDAC5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       membrane;
                                                                                                                    non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            282 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=10716730;
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Rodentia;
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30609
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41.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mitochondrion; Acetylation BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craigen W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB
Pred. No. 27;
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Sciurognathi;
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thi; Muridae; Murinae; Mus
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RESULT 13
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DUN-2002 (Rel. 41, Last annotation update)
Phosphoglycerate kinase (EC 2.7.2.3) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00558; EUKARYOTIC_PORIN; 1.
Outer membrane; Porin; Mitochondrion; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                            Transferase; Kinase; Glycolysis
                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00162; PGK; 1.
PROSITE; PS00111; PGLYCERATE_KINASE; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF001849; AAB58241.1; -. HSSP; P00560; 1QPG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota;
Paramecium
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MOD_RES
                                                                                                                                      259
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                                                                                                                                   PTDFVCGTGLDASSPVALH 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
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7; Conserv
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367 /
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86
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                                                                                                                                                                                                                                          38.1%;
42.1%;
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                                                                                                                                                                                                                                                              Score 40;
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DICYCLOHEXYLCARBODINMIDE (BY SIMILARITY).
MISSING (IN ISOFORM MT-VDAC1).
; C0710C1717063B32 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alberati-Giani D., Buchli R., Malherbe P., Koehler C., Lahm H.-W., Cesura A.M.; "Isolation and expression of a cDNA clone Kynureninase.";
                                                                                                           Hydrolase; Pyridoxal phosphate; Acetylation.

MOD_RES 1 1 PACTIVATION BY SIMILARITY).

BINDING 276 276 PACTIVOXAL PHOSPHATE (BY SIMILARITY).

SEQUENCE 465 AA; 52351 MW; BDD136BE18C79EBB CRC64;
                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extra the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -I- CATALYTIC ACTIVITY: L-kynurenine + H(2)O = a lanine.
-I- CATALYTIC ACTIVITY: L-3-hydroxykynurenine + hydroxyanthranilate + L-alanine.
-I- COFACTOR: PYRIDOXAL PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Kynureninase (EC 3.7.1.3) (L-kynurenine hydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Hepatoma;
MEDLINE=96314506; PubMed=8706755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                               Genew;
                                                                                                                                                                                                                                                                                                                       EMBL; U57721; AAC50650.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eur. J. Biochem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: CATALYZES THE CLEAVAGE OF L-KYNURENINE (L-KYN) AND L-3-HYDROXYKYNURENINE (L-30HKYN) INTO ANTHRANILIC (AA) AND 3-HYDROXYANTHRANILIC ACIDS (3-0HAA), RESPECTIVELY HAS A PREFERENCE FOR THE L-3-HYDROXY FORM. ALSO HAS CYSTEINE-CONJUGATE-BETA-LYASE ACTIVITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENZYME REGULATION: INHIBITED BY O-METHOXYBENZOYLALANINE (OMBA). PATHWAY: INVOLVED IN THE BIOSYNTHESIS OF NAD COFACTORS FROM TRYPTOPHAN THROUGH THE KYNURENINE PATHWAY.
SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFLAMMATORY CONDITIONS.
SIMILARITY: BELONGS TO THE KYNURENINASE FAMILY. SLIGHTLY RELATED CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES TESTED (HEART, BRAIN PLACENTA, LUNG, LIVER, SKELETAL MUSCLE, KIDNEY AND PANCREAS). HIGHEST LEVELS FOUND IN PLACENTA, LIVER AND LUNG. EXPRESSED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: HOMODIMER (BY SIMILARITY) SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INDUCTION: INCREASED LEVELS IN SEVERAL CEREBRAL
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                                                                                                                                                                                                                                   236800;
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                             38.1%;
85.7%;
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                                Pred. No.
                                                        Score 40;
Mismatches
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                                                                                                                  InterPro; IPRO00264; Serum_albumin.
pfam; pF00273; transport_prot; 3.
PRINTS; PR00802; SERUMALBUMIN.
ProDom; PD002486; Serum_albumin; 1.
                                                                                                                                                          EMBL; X60688; CAA43098.1;
EMBL; V00381; CAA23680.1;
PIR; S15571; ABCHS.
HSSP; P02768; 1E7B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-83161037; PubMed=6187737; Hache R.J.G., Wiskocil R., Vasa M., Roy R.N., Lau P.C.K., Deeley R.G. "The 5' noncoding and flanking regions of the avian very low density apolipoprotein II and serum albumin genes. Homologies with the egg
                                                                                    Plasma;
                                                                                                         SMART;
                                                                                                                                                                                                                                                                                                                                                                                proalbumin.";
Biochem. Biophys. Res. Commun.
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MEDLINE=78019943; PubMed=911327;
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15-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biol.
                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: PLASMA.
SIMILARITY: BELONGS TO THE ALB/AFP/VDB
SIMILARITY: CONTAINS 3 ALBUMIN DOMAINS.
                                                                                                                                                                                                                                                                                                                                         BINDING CAPACITY FOR WATER, CA++, NA+, BILIRUBIN AND DRUGS. ITS MAIN FUNCTION COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
                                                                                                                                                                                                                                                                                                                                                                           FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein genes.";
ol. Chem. 258:4556-4564(1983).
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                                                                                                      SM00103; ALBUMIN;
                                                                                   Metal-binding;
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Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                hys. Res. Commun. 78:1060-1066(1977).
SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD APACITY FOR WATER, CA++, NA+, K+, FATTY ACIDS, HORMONES AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               precursor.
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                                                                                 Lipid-binding; Albumin;
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EMBL/GenBank/DDBJ databases.
SERUM AL
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COPPER (
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; Galliformes; Phasianidae; Phasianinae;
                                          ALBUMIN
 (BY SIMILARITY)
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Matches 6
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01-NOV-1997 (Rel. :
15-DEC-1998 (Rel. :
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                                                                                                                                                                                                                                                                                                                     biogenesis and encodes a peroxisomal matrix protein with be carboxy and amino-terminal targeting signals.";
J. Cell Biol. 127:737-749(1994).
-i- FUNCTION: ESSENTIAL FOR PEROXISOME BIOGENESIS. MAY PLAY TRIGGERING THE PROTEIN IMPORT COMPETENCE OF INDIVIDUAL PEROXISOMES. IT MAY INTERACT WITH PER8 (PEX10).
-i- SUBCELLULAR LOCATION: Peroxisomal; matrix.
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pichia angusta (Yeast) (Hansenula polymorpha).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
Saccharomycetales; Saccharomycetaceae; Pichia.
NCBI_TaxID=4905;
    SEQUENCE
                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95050945; PubMed=Waterham H.R., Titorenko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CBS
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                                                                                                                       EMBL; Z30206; CAA82928.1;
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torenko V.I., Ha
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35, Last sequence update
37, Last annotation upda
x protein PER1 precursor
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PEROXISOMAL MATRIX PROTEIN PERI

MICROBODY TARGETING SIGNAL (POT

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atch 38.1%; Score 40; DB 1; Length 650 5al Similarity 36.8%; Pred. No. 64; 7; Conservative 4; Mismatches 8; Indels PVSVGCFVGFDASEPDSRH 19 : : : : : : : : : : : :	1; Length 650; 8; Indels	BB 1; Length 650; ; 8; 8; Indels 0; Gaps 0;
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Maximum Match 100%
Listing first 45 summaries
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SP_Archea:*

Sp_bacteria

Sp_bacteria

Sp_fungl:*

Sp_invert

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105
1 PVSVGCFVGFDASE
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Match
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Gapop 10.0 , Gapext 0.5
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sp_rvirus:*
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      GenCore version 5.1.4_p5_4578 (c) 1993 - 2003 Compugen Ltd.
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      Q9ZT62
Q8WMM7
Q9MMM7
Q9M687
Q9EC87
Q9EC84
Q8ZF926
Q8ZF942
Q8YFH29
Q8YFH29
Q8YFH29
Q9YWD2
Q9YW
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                    Q9zt62 cucumis sat
Q8vwn6 pisum sativ
Q9m4m7 persea amer
Q8u687 agrobacteri
Q9fz85 arabidopsis
Q8uf84 agrobacteri
Q9fnd9 arabidopsis
Q8uf84 agrobacteri
Q9fnd9 arabidopsis
Q8uf84 mrs musculu
Q9ybd2 gallus gall
Q9ybd2 gallus gall
Q9yvw8 rattus sp.
Q49942 mycobacteri
Q9vvq2 drosophila
Q9uvq2 arabidopsis
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    arabidopsis
arabidopsis
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Matches 19; Conserv
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PHELLIALLIA

O92T62;
O92T62;
O1-MAY-1999 (TrEMBLrel. 10, Created)
O1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
O1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
O1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
  Q8VWN6;
Q8VWN6;
Q1-MAR-2002
Q1-MAR-2002
Q1-MAR-2002
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Obsumi C., Nozaki J., Kida T.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF073744; AAD02832.1;
Clycosyltransferase; Transferase.
SEQUENCE 784 AA; 86920 MW; 3B06A491F0908933 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cucumis sativus (Cucumber).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3659;
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                                                                                                                                                                                                                            1 PVSVGCFVGFDASEPDSRH 19
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Q9FVH5
Q9LCH6
Q08410
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Q51720
Q9XW86
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Q9GZF1
Q8R0F7
Q92P85
Q23053
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Q971E6
Q9MCH9
Q9U249
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Last sequence update)
Last annotation update)
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Pred. No. 7.7e-09;
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09av10 oryza sativ
0942t6 oryza sativ
0971e6 sulfolobus
0971e6 sulfolobus
0971e6 sulfolobus
0971e6 sulfolobus
0971e6 sulfolobus
0971e7 saenorhabdi
09xeq8 sorghum bic
094892 thermoplasm
094ay8 arabidopsis
09grf1 caenorhabdi
08r0f7 mus musculu
092p85 rhizobium m
023053 arabidopsis
09cxf0 mus musculu
031813 bacillus su
09yb34 aeropyrum p
09kbf5 bacillus su
09yb34 aeropyrum p
09kbf5 caenorhabdi
04789 caenorhabdi
048910 caenorhabdi
048710 proplonibac
09xw86 caenorhabdi
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Gaps

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RESULT
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                              01-JUN-2002 (TrEMBLrel. 21, Cre
01-JUN-2002 (TrEMBLrel. 21, Las
01-JUN-2002 (TrEMBLrel. 21, Las
Hypothetical protein Atu6048.
ATU6048 OR AGR_PTI_100.
                                                                                                 Q8U687;
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           Bacteria;
                                                                                                                                                                                                                                                         cold storage of avocado (Persea americana Mill Submitted (MAR-1999) to the EMBL/GenBank/DDBJ EMBL; AJ133148; CAB77245-1; - C3A8B4316031678
                                                                                                                                                                                                                                                                                                            STRAIN=CV. HASS; TISSUE=MES Zamorano J.P., Evans A.D., Merodio C., Grierson D.;
                                                                                                                                                                                                                                                                                                                                                                             Persea americana (Avocado).
Eukaryota; Viridiplantae; Streptophyta;
Spermatophyta; Magnoliophyta; Laurales;
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STRAIN-CV. WUNDER VON KELVEDON; TISSUE-SEED;

Peterbauer T., Mach L., Mucha J., Richter A.;

"Molecular characterization of raffinose synthase from pea sativum L.) seeds.";

Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ426475; CAD20127.2; -.

Transferase; Glycosyltransferase.

SEQUENCE 798 AA; 88717 MW; 8D3F3ED5BF8617B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Raffinose
RFS.
                                                                                                                                                                                                                                                                            "Isolation and characterization of cDNAs for mRNAs regulated cold storage of avocado (Persea americana Mill.) fruit."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; NCBI_TaxID=3888;
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                    pTiC58.
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          Proteobacteria;
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60.0%;
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21, Last sequence update)
21, Last annotation updat

    Last sequence update)
    Last annotation updat protein.

           alpha
                                (strain C58
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           subdivision;
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                                 ATCC 33970).
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9.7;
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           Rhizobiaceae
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          group;
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RESULT
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SEQUENCE FROM N.A.
Yamada K., Banh J., Char
Yamada K., Bonh J., Char
Lee J.M., Onodera C.S.,
Yamamura Y., Yu G., Yu S
Hayashizaki Y., Ishida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9FZ85;
Q9FZ85;
01-MAR-2001
01-MAR-2001
01-JUN-2002
                                                                                                                                                 SEQUENCE FROM N.A.

SEQUENCE FROM N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F., Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F., Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks Buehler E., Chao Q., Chin C., Chiou J., Choi E., Gonzalez A., Howng B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M., Lenz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Shir Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis F. Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphatase).
F26II6.2 OR ATIG18640.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., M Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Mar Filanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Alneida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M. Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M. Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Nester E.W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE009423; AAL46284.1; -.
EMBL; AE007931; AAK91006.1; -.
Hypothetical protein; Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of the plant Agrobacterium tumefaciens C58. Science 29:2323-2328(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=21608551; PubMed=11743194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The
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                                                                                                                                                                                                                                                                                                                                                                                                                       II; Brassicales;
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Chang C.H., Chang E., Dale J.M.,
S., Quach H.L., Tang C., Toriumi
Yu., Bowser L., Carninci P., Ci
ida J., Jones T., Kamiya A., Karli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91964 MW;
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eudicots; Rosidae;
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hen H., Cheuk R.,
                                                                           Goldsmith A.D.,
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
11-JUN-2002 (TrEMBLrel. 21, Last annotation update)
12-JUN-2002 (TrEMBLrel. 21, Last annotation update)
13-JUN-2002 (TrEMBLrel. 21, Last annotation update)
14-JUN-2002 (TrEMBLrel. 21, Last sequence update)
15-JUN-2002 (TrEMBLrel. 21, Last sequence update)
15-JUN-2002 (TrEMBLrel. 21, Last sequence update)
15-JUN-2002 (TrEMBLrel. 21, Created)
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15-JUN-2002 (TrEMBLrel. 21, Last sequence update)
15-JUN-2002 (TrEMBLrel. 21, Last sequence update)
16-JUN-2002 (TrEMBLrel. 21, Last sequence update)
17-JUN-2002 (TrEMBLrel. 21, Last sequence update)
18-JUN-2002 (TrEMBLrel. 21, Last seq
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Interpro; IPR004469; SerB.
Pfam; PF00702; Hydrolase; 1.
TIGRFAMS; TIGR00338; SerB; 1.
SEQUENCE 295 AA; 32318 MW; F14C95E
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EMBL; AY065351; AAL38792.1; -
NCBI_TaxID=176299; [1]
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SEQUENCE 295 AA; 32302 MW;
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Pfam; PF00702; Hydrolase; 1.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Narusaka M.,
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Southwick A., Sh
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Palm C.J., Sakurai T., Sal
Shinozaki K., Davis R.W.,
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MEDILINE-21608550; PubMed-11743193;

WOOD D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

Wood D.W., Setubal J.C., Kaul R., Monks D.E., Almeida N.F. Jr., Woo L.

Chen Y., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.

Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Kaymond C., Rouse G., Saenphimmachak C., W.Z., Romero P., Gordon

Kaymond C., Tao Y., Biddle P., Jung M., Krespan W., Perry

Gordon Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan

Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
SEQUENCE FROM N.A.
Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
Ecker J., Theologis A., Davis R.W.;
                                                                                                                    DNA
[2]
                                                                                                                              "Structural analysis of A
Sequence features of the
physically assigned P1 clu
DNA Res. 4:291-300(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mul Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F. Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Mark Wollam C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.
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                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo; Spermatophyta; agnoliophyta; eudicotyledons; core eudicots; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                 Q9FND9;
01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cielo C., Slater S.;
"Genome sequence of the plant pathogen Agrobacterium tumefactens C58.";
Science 294:2323-2328(2001).
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 Q8VEA8;
Q8VEA8;
01-MAR-2002
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Q8YFH2;
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MEDLINE=20020109; PubMed=11756688;

MEDLINE=20020109; PubMed=11756688;

DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.

IVanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,

Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.

Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,

Haselkorn R., Kyrpides N., Overbeek R.;
                                                                                                                                                                                                                                                                       InterPro; IPR005289; GTP-bindding_dom.
InterPro; IPR002917; MMR_HSR1.
InterPro; IPR005225; Small_GTP.
Pfam; PP01926; MMR_HSR1; 1.
TIGRFAMS; TIGR00650; MG442; 2.
TIGRFAMS; TIGR00231; small_GTP; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                       "The genome sequence of the facultative intracellular pathogen Brucella melitensis.";
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Bacteria; Proteobacteria;
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Q9YHD2;
Q9YHD2;
01-MAY-1999
01-MAY-1999
01-JUN-2002
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01-MAY-1999 (TrEMBLrel. 10,
01-JUN-2002 (TrEMBLrel. 21,
Nuclear calmodulin-binding p
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01-JUN-2002 (TrEMBLrel. 21, La
Hypothetical 22.5 kDa protein.
Mus musculus (Mouse).
                                                                                                                                                                           InterPro; IPR003878; SPRY_domain.
InterPro; IPR003877; SPRY_receptor.
Pfam; PF00622; SPRY_ 1.
                                                                                                                                                                                                                                   Submitted (OCT-1998) to the EMBL/GenBank/DDBJ EMBL; aF098788; aAC69888.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                  Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein. SEQUENCE 199 AA; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00175; RAB; 1.
PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00071; ras; 1.
PRINTS; PR00449; RASTRNSFRMNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; BC019395; AAH19395.1; -.
InterPro; IPR003579; GTPase_Rab.
InterPro; IPR001806; Ras_trnsfrmng.
                                                                                                                                                                 SMART; SM00449; SPRY; 1.
                                                                                                                                                                                                                                                                  to HnRNP-U.";
                                                                                                                                                                                                                                                                              Lodge A.P., Walsh A., McNamee C.J., "Identification of ChURP, a Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000834; Zn_carbOpept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 7; Conser
                               4 VGCFVGFDASEPD
IGCFADFEASEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDGCILAFDVTDPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVGCFVGFDASEPDS 17
                                                              . Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FROM N.A.
                                                                                                                                  757
                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                  AA;
354
                                16
                                                                                                                                                                                                                                                                                                                                                                                                    Neognathae;
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                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                  84179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22502 MW;
                                                                                 42.9%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.98;
46.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20, Last sequence update)
21, Last annotation updat
                                                                                                                                  MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein (Fragment).
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last annotation update)
                                                                                 Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33353842079CF6FC CRC64;
                                                                                                                                  7FA04ED9E1776D1D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                Mismatches
                                                                                                                                                                                                                                                                                 Moss D.J.;
Calmodulin-Binding Protein
                                                                                   64;
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                                                                                                 DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 11;
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                                                                                                 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                    databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4;
                                                                                               Length 757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 199;
                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                0;
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                                                                Gaps
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PRELIMINARY;

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204942
AC 000 DT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ş
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Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-1128732; PubMed-11234002;
Gole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Wheeler R., Basham D., Brown D., Chillingworth T., Connor R.,
Mungall K., Basham D., Brown D., Chillingworth T., Fraser A., Hamlin N.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quall M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q49942;
Q49942;
                                       Smith D.R., Robison K.;
Submitted (MAY-1998) to the
EMBL; AL583925; CAC31862.1;
EMBL; U00023; AAA17366.1; -
EMBL; AL023596; CAA19144.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
Hypothetical protein ML2346.
ML2346 OR L518_F3_81 OR MLCB2407.04.
Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 01-MAY-2000 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                           "Massive gene decay in the Nature 409:1007-1011(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Squares S., S
Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Actinomycetales;
NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00107; PROTEIN_KINASE_ATP;
PROSITE; PS00111; PROTEIN KINASE_ATP;
ATP-hind-i-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yazaki N., Hosoi Y., Kawabata K., Miyake A., Minami M., Ohta M., Kawasaki T., Itoh N.; "Differential expression patterns of mRNAs for members of the control                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-94293355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-10118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P11362;
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9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corynebacterineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19; Euk_pkinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37:445-452(1994).
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21986 MW;
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13, Last sequence update)
21, Last annotation update)
receptor 4, FGFR-4 (Fragment).
                                                                                                                                                                                the
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                                                                                                                                                                                                                                                                                                                                                                                                                       leprosy bacillus.";
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Last annotation update)
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3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Satoh
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RESULT 14
Q9VVQ2
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                                                             Adams M.D., Celliker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celliker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Sutton G.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RS Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RS Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklog G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklog G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., By Bhandari D., Bolshakov S.,
RA Borkva D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Bortkva D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Bortkva D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Bortkva D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Bortkva D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Bortkva D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Bortkva D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Bortkva D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Bortkva D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Bortkva D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Dodson K., Doup L.E., Downes M., Dupan-Rocha S., Dunkov B.C., Dunn P.,
RA Grots A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Dutbin K.J., Evaltsky A.A., Li J., Li R., Huuk J.,
RA Glodek A., Gong F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Harris N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Hostin D.R., Nelson K.A., Nixon K., Nusskern J.A., Nestechum K.A.,
RA Hulliam G.S., Pan S., Pollard J., Messen D.L.,
RA Hostin D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Hulliam R.S., Kenington K.S., Sanders R.D., Scheeler F., Shen H.,
RA Shie B., C., Scheler S., Walley K., Walley B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Q9VVQ2;
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01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein; Complete proteome. SEQUENCE 301 AA; 33939 MW; CF11EF2EEAE7AOAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Tracheata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CG7271 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20196006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200
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                                                        FBgn0036791;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                      47361 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41.9%;
57.1%;
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 44; DB Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fly)
                                      F0519C00EFAA569C CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
Length 421;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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41.98;

Score 44;

DB

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RESULT 15
Q9LZ54
ID Q9LZ55
AC Q9LZ5
AC Q9LZ5
DT 01-QC
DT 01-QC
DT 01-QC
DT 01-QC
CT
GN T22P1
QOC Sperma
QC Sperma
QC Sperma
QC SPERMA
QC NCBI_
RN [1]
RP SEQUE
RA Bancar
RA Bancar
RA Bancar
RA Submi
RN [2]
RP SEQUE
RA SUBMi
RN [1]
RP SEQUE
RA BANCAT
RA SUBMI
RN [2]
RP SEQUE
RA SUBMI
RN [2]
RP SEQUE
RA SUBMI
RN [1]
RN [1]
RN [1]
RN SEQUE
RA SUBMI
RN [1]
RN SUBMI
RN [1]
RN SUBMI
Search completed: March 27, Job time: 13.6585 secs
                                                                                               В
                                                                                                                                         Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                     Query Match 41.9
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 50.0%; Matches 7; Conservative
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

BU Arabidopsis sequencing project;

BU Arabidopsis sequencing project;

Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AL162971; CAB85985.1; -

InterPro; IPR002068; Hsp20.

InterPro; IPR000834; Zn_carbOpept.

PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_1.

PROSITE; PS01031; HSP20; 1.

Hypothetical protein.

SEQUENCE 498 AA; 55530 MW; 0791437EB8817BE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O9LZ54 PRELIMINARY; PRT; 498 AA.
09LZ54; O1-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 55.5 kDa protein.
T22P11_70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
Bancroft I., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                             5 GCFVGFDASE 14
||| ||| |:
132 GCFTGFDKSD 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 CYSSIDADEPPSQH 49
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                                                                                                                                                                                                                41.98;
70.08;
                           2003, 10:05:59
                                                                                                                                                                                     Score 44; DB 10; Length 498;
Pred. No. 61;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 51;
2; Mismatches
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                                                                                                                                                                                          0;
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq
     Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/U
2: /cgn2_6/ptodata/2/pubpaa/U
3: /cgn2_6/ptodata/2/pubpaa/U
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14: /cgn2_6/ptodata/2/pubpaa/U
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length: 2000000000
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105
1 PVSVGCFVGFDASEPDSRH
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Match
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         March 27, 2003, 10:04:25; Search time 4.40244 Seconds (without alignments)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      237916 seqs, 58723674 residues
     : /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep: *
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: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep: *
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                                                                                                                                                                                                                                                                                                                                           Length
   10 US-09-873-880-34

10 US-09-873-880-36

3 US-09-738-6264-4094

10 US-09-924-256A-34

10 US-09-924-256A-34

10 US-10-081-806-6

3 US-10-081-806-6

3 US-10-074-328-6

3 US-09-940-224-6

3 US-09-940-224-6

3 US-09-940-235-6

3 US-09-777-430A-8

4 US-09-777-430A-15

5 US-09-777-430A-20

6 US-09-777-430A-20

7 US-09-777-430A-20

7 US-09-777-430A-20

8 US-09-777-430A-21

8 US-09-777-430A-23

8 US-09-777-430A-23

8 US-09-777-430A-23

8 US-09-813-153-11
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                 Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 259, Appli
Sequence 259, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 26, Appli
Sequence 26, Appli
Sequence 26, Appli
                                                                                                                                                                                                                                     Sequence 34, Appl
Sequence 36, Appl
Sequence 4094, Ap
Sequence 22, Appl
Sequence 34, Appl
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Sequence Sequence

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RESUUS-0 US-0 ; Se ; Pa ; GE ; A	Дy	Ma Be	RESUUS-OUS-OUS-OUS-OUS-OUS-OUS-OUS-OUS-OUS		
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lon US 18A1 Incent Carl Carl)SR 18 - SR 22	42. 50. ative	ilion US/ iliani incent Carl Carl Carl CYCINE 92 US C NUMBER: NUMBER: NUMBER: OUT 28, NUMBER: Office		833 833 143 233 2440 440 4410 4410 831 831 831 831 831 831 831 831 831 831
E. M.	42	9,9	% 098: CIP CIP CIP 8: US, 19/3: , 19/3: , 19/3: , 19/3:		000000000000000000000000000000000000000
ion US/09873880 118A1 'Incent '. Carl tephen M. GLYCINE-METABOLISM ENZYMES		Score 45; DB 10; Length Pred. No. 12; 4; Mismatches 4; Inde.	/09873880 M. E METABOLISM ENZYMES CIP -06-04 09/363,321 09/363,321 (1999 60/094,839 , 1998	ALIGNMENTS	US-10-081-806-8 US-10-074-328-8 US-09-940-244-8 US-09-940-925A-8 US-09-894-998-11 US-09-83-450-20 US-09-83-450-20 US-09-83-955-3 US-09-838-955-3 US-09-9894-998-12 US-10-031-297-5 US-10-031-297-5 US-10-074-328-5 US-09-940-925A-5 US-09-940-925A-5 US-09-940-925A-5 US-09-941-39A-12 US-09-813-148-3 US-09-8
		ngth 296; Indels 0; Gaps			Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 11, Appl Sequence 11, Appl Sequence 20, Appli Sequence 20, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 3, Appli Sequence 375, Appli Sequence 375, Appli Sequence 23, Appli Sequence 23, Appli Sequence 23, Appli Sequence 24, Appli Sequence 27, Appli Sequence 27, Appli Sequence 28, Appli Sequence 20, Appli Sequence 3981, Appli
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RESULT 4
US-09-924-256A-22
: Sequence 22, Application US/09924256A
: Patent No. US20020127659A1
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                                                                                                                                                                                                                                                                                          ; SEQ ID NO 4094
; LENGTH: 382
; TYPE: PRT
; ORCANISM: Corynebacterium glutamicum US-09-738-626-4094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT ; ORGANISM: Oryza sativa US-09-873-880-36
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US-09-738-626-4094
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GENERAL INFORMATION:
APPLICANT: Waters, Barba
APPLICANT: Miao, Vivian
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Microsoft Office 97 SEQ ID NO 36
                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/363,321
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: 60/094,839
PRIOR FILING DATE: July 31, 1998
NUMBER OF SEQ ID NOS: 42
                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: BB1192 US CIP
CURRENT APPLICATION NUMBER: US/09/873,880
CURRENT FILING DATE: 2001-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: JP 00/159162 PRIOR FILING DATE: 2000-04-07
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                                                                                                                                                       249
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nes 8; Conserv
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OCHIAI, KEIKO
YOKOI, HARUHIKO
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SENOH, AKIHIRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IKEDA, MASATO
                                                                                                                                                                                                                           Conservative
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57.18;
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    Mismatches

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Pred. No.
                                                                                                                                                                                                                                                          Score 42;
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24;
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; SEQ ID NO 34
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Leptogium corniculatum
US-09-924-256A-34
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                                                                                                                                                   US-10-033-297-6
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; Sequence 34, Ap
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LENGTH: 212
TYPE: PRT
                                                                                                                Sequence 6, Application US/10033297 Publication No. US20020187486A1
                                                                                                                                                                                                                                                                                                         Best Local Similarity Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                              Query Match
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/924,256A CURRENT FILING DATE: 2001-08-08 PRIOR APPLICATION NUMBER: 08/861,774 PRIOR FILING DATE: 2001-04-13 NUMBER OF SEQ ID NOS: 94 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: TONG, SECW TITLE OF INVENTION: METHOD FOR ISOLATION OF BIOSYNTHESIS GENES FOR TITLE OF INVENTION: BIOACTIVE MOLECULES FILE REFERENCE: 9993-006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Waters, Barbara APPLICANT: Miao, Vivian APPLICANT: Ho, Yap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 08/861,774
PRIOR FILING DATE: 2001-04-13
NUMBER OF SEO ID NOS: 94
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/924,256A CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Tong, Seow
TITLE OF INVENTION: METHOD FOR ISOLATION OF BIOSYNTHESIS GENES
TITLE OF INVENTION: BIOACTIVE MOLECULES
FILE REFERENCE: 9993-006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: SITE
LOCATION: (136)
OTHER INFORMATION: Xaa-unknown amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Xanthoparmelia cumberlandia FEATURE:
                                                                                                                                                                                                                                  22 PEDVGCYIGACATDYD 37
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     TITLE OF
                                                                            APPLICANT: Hall,
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Mast, Andrea L.
Brow, Mary Ann D.
INVENTION: Detection Of Nucleic Acids
                                                         Hall, Jeff G.
Lyamichev, Victor
                                                                                                                                                                                                                                                                                                                            39.0%;
43.8%;
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43.8%;
                                                                                                                                                                                                                                                                                                                            Score 41;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                            Length 212;
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STREET: 220 Montgomery Street, Suite 2200

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; MOLECULE TYPE: protein;
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-033-297-6
                                                                                                                                                                                                            US-10-081-806-6
                                                                                                                                                                                                                                 RESULT 7
                                                                                                                                             Sequence 6, Application US/10081806 Publication No. US20020197623A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                38.1%;
Local Similarity 61.5%;
les 8; Conserva++...
                                                                                                                                                                                                                                                                                            64 FVVFDAKAPSFRH 76
                                                                                                                                                                                                                                                                                                                                  7 FVGFDASEPDSRH 19
                                              Hall, Jeff G.
Lyamichev, Victor I.
TITLE OF INVENTION: Invasive Cleavge Of Nucleic NUMBER OF SEQUENCES: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 40,027
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FOI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94104
COMPUTER READABLE FORM:
                             CORRESPONDENCE
                                                                                                                            APPLICANT: Prudent, James R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/823,516
FILING DATE: 24-MAR-1997
APPLICATION NUMBER: PCT/US97/01072
FILING DATE: 21-JAN-1997
APPLICATION NUMBER: US 08/759,038
FILING DATE: 02-DEC-1996
APPLICATION NUMBER: US 08/758,314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/10/033,297
FILING DATE: 12-No. US20020187486A1-2001
CLASSIFICATION: CUNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 834 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/682,853 FILING DATE: 12-UUL-1996 APPLICATION NUMBER: US 08/599,491 FILING DATE: 24-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 02-DEC-1996
APPLICATION NUMBER: US 08/756,386
FILING DATE: 29-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      United States Of America
ADDRESS:
: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         397-8338
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Pred. No. 2.2e+02;
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RESULT 8
US-10-074-328-6
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Matches
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 FVVFDAKAPSFRH 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 FYGFDASEPDSRH 19
                                                                    ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                   GROTELUESCHEN HALL, JEFF S.

LYAMICHEV, VICTOR

OLIVE, DAVID M.

PRUDENT, JAMES R.

PRUDENT, JAMES R.

TITLE OF INVENTION: DETECTION OF NUCLEIC ACID
INVADER-DIRECTED CLEAVAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FO'
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/599,491
FILING DATE: 24-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CURRENT APPLICATION DATA:
                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA
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                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 61.5
8; Conservative
            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/10074328
                                                                                                                                                                        STREET: 220 MONTGOMERY CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/10/081,806 FILING DATE: 22-Feb-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                      STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/756,386
FILING DATE: CUNKNOWN>
APPLICATION NUMBER: US 08/682,853
FILING DATE: 12-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                 COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 834 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                 US20030013098A1
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                                                                                                                                                                                                                                                                                                                                                                                           BROW, MARY ANN D.
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Pred. No. 2
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2.2e+02;
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FILE REFERENCE: FORS-06478

CURRENT APPLICATION NUMBER: US/09/940,244

CURRENT FILING DATE: 2002-05-06

NUMBER OF SEQ ID NOS: 422

SOFTWARE: PatentIn version 3.1

SEQ ID NO 6

LENGTH: 834

TYPE: PRT
ORGANISM: Thermus thermophilus
US-09-940-244-6
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                                                                                                                                                                   US-09-940-925A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-10-074-328-6
                                                                                                       Sequence 6, Application US/09940925A Publication No. US20030054338A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/09940244 Publication No. US20030044796A1 GENERAL INFORMATION:
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Best Local Similarity 61.5%;
Matches 8; Conservative
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APPLICANT: Hall, Jeff G.
APPLICANT: Lyamichev, Victor
APPLICANT: Smith, Lloyd M.
TITLE OF INVENTION: Reactions on Dendrimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 834 amino acids
                                                                                                                                                                                                                                          64 FVVFDAKAPSFRH 76
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Local Similarity 61.5%;
les 8; Conservation
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                            APPLICANT: BROW, MARY ANN D.

LYAMICHEV, VICTOR I.

OLIVE, DAVID M.

TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/599,491 FILING DATE: 23-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: INGOLIA, DIANE E. REGISTRATION NUMBER: P-40,027
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SEQUENCES:
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               PATHOGENS
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Pred. No.
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Neri, Bruce P.
APPLICANT: Hall, Jeff G.
APPLICANT: Lyamichev, Victor
APPLICANT: Smith, Lloyd M.
                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.1
SEQ ID NO 259
LENGTH: 836
                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 8; Conserv
                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 259, A Publication No.
                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/940,244
CURRENT FILING DATE: 2002-05-06
NUMBER OF SEQ ID NOS: 422
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Smith, Lloyd M.
TITLE OF INVENTION: Reactions on Dendrimers
FILE REFERENCE: FORS-06478
                                                                                                                                                                                 ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 397-
INFORMATION FOR SEQ ID NO: 6:
                                                                       Local Similarity
nes 8; Conserv
66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 FVVFDAKAPSFRH
                                   7 FVGFDASEPDSRH 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 FVGFDASEPDSRH 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/940,925A
FILING DATE: 10-Jun-2002
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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ADDRESSEE: MEDLEN & CARROLL
STREET: 20 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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 FVVFDAKAPSFRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           259,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-01756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                       Conservative
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   78
                                                                                        38.1%;
61.5%;
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                                                                     Score 40; DB 9; Lc
Pred. No. 2.2e+02;
""" matches 5;
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Pred. No. 2.2e+02;
"'~matches 5;
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APPLICANT: Takova, Teetska

APPLICANT: Neir, Bruce P.

TITLE OF INVENTION: Charge Tags and the Separation of Nucleic Acid Molecules

FILE REFERENCE: FORS-04912

CURRENT APPLICATION NUMBER: US/09/777,430A

CURRENT FILING DATE: 2001-02-06

NUMBER OF SEQ ID NOS: 85

SOFTWARE: PatentIn version 3.1

SEQ ID NO 8

LENGTH: 836

TYPE: PRT

ORGANISM: Thermus thermophilus

US-09-777-430A-8
                                                                                                                                                                                                                                                                                                      APPLICANT: Neir, Bruce P.

TITLE OF INVENTION: Charge Tags and the Separation of Nucleic Acid Molecules
FILE REFERENCE: FORS-04912
CURRENT APPLICATION NUMBER: US/09/777,430A
CURRENT FILING DATE: 2001-02-06
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin version 3.1
SEQ ID NO 11
LENGTH: 836
TYPE: PRT
ORGANISM: Thermus thermophilus
US-09-777-430A-11
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US-09-777-430A-8
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US-09-777-430A-11
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Sequence 15, Application US/09777430A
Patent No. US20020128465A1
GENERAL INFORMATION:
APPLICANT: Lyamichev, Victor
APPLICANT: Skrzypczynski, Zbigniew
APPLICANT: Allawi, Hatim T.
                                                                                                                                                                                                                                                Best Loc
Matches
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APPLICANT: Lyamichev, Victor
APPLICANT: Skrzypczynski, 21
APPLICANT: Allawi, Hatim T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/09777430A Patent No. US20020128465A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                Query Match
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APPLICANT: Skrzypczynski, Zi
APPLICANT: Allawi, Hatim T.
APPLICANT: Wayland, Sarah R
APPLICANT: Takova, Tsetska
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les 8; Conserv
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les 8; Conservative
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Allawi, Hatim T.
Wayland, Sarah R.
Takova, Tsetska
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61.5%;
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Pred. No. 2.2e+02;
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Pred. No. 2.2e+02;
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CURRENT APPLICATION NUMBER: US/09/777,430A
CURRENT FILING DATE: 2001-02-06
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin version 3.1
SEQ ID NO 15
LENGTH: 842
TYPE: PRT
ORGANISM: Thermus thermophilus
US-09-777-430A-15
Search completed: March 27, Job time: 5.40244 secs
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US-09-777-430A-20
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SEQ ID NO 20
LENGTH: 842
TYPE: PRT
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                 Query Match
Best Local
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APPLICANT:
                                                                                                                                  Matches
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APPLICANT: Takova, Tsetska
APPLICANT: Neir, Bruce P.
TITLE OF INVENTION: Charge Tags and the Separation of Nucleic Acid Molecules
FILE REFERENCE: FORS-04912
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lyamichev, Victor APPLICANT: Skrzypczynski, Z
                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Charge Tags and the Separation of Nucleic Acid Molecules FILE REFERENCE: FORS-04912
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                   66
                                                                                                                               Local Similarity 61.
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                                                                   FVVFDAKAPSFRH
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Allawi, Hatim T.
Wayland, Sarah R.
Takova, Tsetska
Neir, Bruce P.
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Pred. No. 2.
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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US-07-830-330-1
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ALIGNMENTS

US-08-846-234-1 Sequence 1, Application US/08846234 Patent No. 6166292 GENERAL INFORMATION: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, VG CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/846,234 FILING DATE: ATTORNEY/AGENT INFORMATION: TELEPHONE: (703)-413-3 TELEFAX: (703)-413-222 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: ENERAL INFURMATION. APPLICANT: OSUMI Chieko APPLICANT: NOZARI Jinshi APPLICANT: KIDA Takao TITLE OF INVENTION: RAFFINOSE SYNTHASE GENE, TITLE OF INVENTION: PRODUCING RAFFINOSE, AND NUMBER OF SEQUENCES: 22 CORRESPONDENCE ADDRESS: ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR MOLECULE TYPE: FRAGMENT TYPE: REGISTRATION NUMBER: 24,618 TELECOMMUNICATION INFORMATION: TELEPHONE: (703)-413-3000 STREET: 1755 S. CITY: ARLINGTON STATE: VIRGINIA COUNTRY: USA ZIP: 22202 TOPOLOGY: TYPE: NAME: NORMAN F. OBLON LENGTH: amino acid 30 amino acids (703)-413-2220 linear peptide internal Version #1.30 (EPO) METHOD FOR TRANSGENIC PLANT

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FGWCTWDAFYLTVHPQGVIEGVRHLVDGGC 30 FGWCTWDAFYLTVHPQGVIEGVRHLVDGGC

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US-08-846-234-1

Query Match
Best Local Similarity
Matches 30; Conserv

100.0%; llarity 100.0%; Conservative 0

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Patent No. 616629
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[NFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 784 amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                APPLICANT: OLSON, PAMELA
APPLICANT: OLSEN, DAVID
APPLICANT: CARRILLO, PEDRO A.
TITLE OF INVENTION: POLYPEPTIDE FUSIONS TO
TITLE OF INVENTION: INTERLEUKIN-1-LIKE POLYPEPTIDES
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)-413-3000
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ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: RAFFINOSE SYNTHASE GENE, METHOD FOR TITLE OF INVENTION: PRODUCING RAFFINOSE, AND TRANSGENIC NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
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TOPOLOGY:
                                                                     COUNTRY: USA
ZIP: 94304-1018
                                                                                                         CITY: Palo Alto
STATE: California
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ZIP: 22202
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                                                                                                                                                                ADDRESSEE:
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GY: linear
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ZHANG, SUNNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                               INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                             REFERENCE/DOCKET NUMBER: 22: TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                         ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: PARK, FREDDIE K.
REGISTRATION NUMBER: 35,
                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Rele
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 02-AUG-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: EXPRESSION OF FUSION POLYPEPTIDES
TITLE OF INVENTION: TRANSPORTED OUT OF THE CYTOPLASM WITHOUT LEADER SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                  TELEPHONE: (415) 494-0792
                                                                                                                                                                                                                          APPLICATION NUMBER: US/0 FILING DATE: 02-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 494-0792
                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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les 10; Conserv
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 STRANDEDNESS:
                               LENGTH:
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                amino acid
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                                                                                                                                                                                                                                                                                                                                                                                         California
                          132 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                           755 Page Mill Road
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VENTION: EXPRESSION OF FUSION POLYPEPTIDES
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OLSON, PAMELA S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MASCARENHAS, DESMOND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                           MORRISON & FOERSTER
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US-08-854-811-4
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RESULT 6
PCT-US90-06962-1
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                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
STRANDEDNESS: $10017
                                                                                                                          Query Match
Best Local Similarity
Matches 10; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/854,811
FILING DATE: 12-MAY 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/284,784
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/100,744
FILING DATE: 02-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: ITITLE OF INVENTION: ITITLE OF INVENTION: ITITLE OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                NAME: Buffinger, Nicholas S
REGISTRATION NUMBER: 39,124
REFERENCE/DOCKET NUMBER: 200
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: Windows Version 2.0b SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 02-AUG-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 755 PAGE
CITY: Palo Alto
                                                             10 YCKNGGFFLRIHPDGRVDGVREKSD 34
                                                                                                                                                                                                                                                                                                  TELEPHONE: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER:
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Local Similarity 40.0%;
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                                                                                                                                       Score 60; DB 2; Length 132; Pred. No. 0.17;
                                                                                                                      5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                 22095-20275.21
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Pred. No. 0.
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US-07-830-330-1
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Best Local Similarity 40.0%;
Matches 10; Conservative
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                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
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LENGTH: 157 amino acids
TYPE: AMINO ACID
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 507
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)552-1311
TELEFAX: (619)552-0095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US OF STILING DATE: 30-NOW1109 ATTORNEY/AGENT INFORMATION: NAME: Schumann, James J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Baird, J. A.
APPLICANT: Hajjar, David P.
TITLE OF INVENTION: Treatment of HSV
                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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CITY: Chicago
STATE: Illinois
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ZIP: 606
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                                                        STATE: Virginia
ZIP: 22202
                                                                                           STREET: 1755 Jefferson Davis Highway, Fourth Floor CITY: Arlington
                                                                                                                                ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35 YCKNGGFFLRIHPDGRVDGVREKSD 59
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135 South LaSalle Street, Suite 900
                                                                                                                                                                                                                                                                               Garofano, Luisa
Battistini, Carlo
Carminati, Paolo
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                     FOR USE AS ANTIVIRAL AGENT
                                                                                                                                                                                                                        SYNERGISTIC COMPOSITION COMPRISING A FIBROBLAST GROWTH FACTOR AND A SULFATED POLYSACCHARIDE.
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US-08-187-780-3
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TELECOMMUNICATION INFORMATION:
TELEPAN: (703)521-4500
TELEPAX: (703)466-2347
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application Patent No. 5459250 GENERAL INFORMATION:
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         FILING DATE: December 6, 1991
APPLICATION NUMBER: 07/17,50
FILING DATE: April 4, 1988
APPLICATION NUMBER: 07/062.92
FILING DATE: June 16, 1987
ATTORNEY_AGENT INFORMATION:
NAME: HOWAT M. FIRINKOTT
REGISTRATION NUMBER: 32,613
                                                                                                         PRIOR APPLICATION NUMBER: 07/you, APPLICATION NUMBER: 07/806,771 APPLICATION NUMBER: 07/806,771 PRIVING DATE: December 6, 1991 PRIVING DATE: NUMBER: 07/177,506
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25
MEDIUM TYPE: 360 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: CLAUDIO BASILICO
APPLICANT: DANIELA TALARICO
TITLE OF INVENTION: MAMMALII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/187,780
FILING DATE: January 25, 1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5288704man F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Rel-
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24
 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM or IBM-compatible OPERATING SYSTEM: PC/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 19920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 WCTWDAFYLTVHPQGVIEGVRHLVD 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YCKNGGFFLRIHPDGRVDGVREKSD 48
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40.0%;
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                                                                                           07/062,925
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5986/13586-053
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Pred. No. 0.19;
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application Patent No. 5883071
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                            MEDIUM TYPE: Floppy Diskette,
MEDIUM TYPE: 1.44 MB storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                           FILING DATE: Concurrently Herev
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,780
                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: CLAUDIO BASILICO
APPLICANT: DANIELA TALARICO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUBLICATION INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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STATE: New Yor
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STRANDEDNESS: sir
                                FILING DATE:
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APPLICATION NUMBER: 0 FILING DATE: June 22,
                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS:
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               January 25, 1994
UMBER: 07/901,705
                                                                                              Concurrently Herewith
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                                                                                                             US/08/478,485
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Pred. No. 0.19;
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RESULT 10
US-08-478-486F-3
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REFERENCE/DOCKET NUMBER: 5986
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEPACE: (212) 753-637
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                            Sequence 3, Application US/08478486F Patent No. 6432702 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local 9
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FILING DATE: December 6, 199
APPLICATION NUMBER: 07/17,5
FILING DATE: April 4, 1988
APPLICATION NUMBER: 07/062,5
FILING DATE: June 16, 1987
ATTORNEY/AGENT INFORMATION:
NAME: JOSEPH R. ROBINSON
NAME: JOSEPH R. ROBINSON
                                                                                                                                          APPLICANT: CLAUDIO BASILICO
APPLICANT: DANIELA TALARICO
TITLE OF INVENTION: MAMMALIAN GRC
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby P.C.
STREET: 805 Third Avenue
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Diskette,
MEDIUM TYPE: 1.44 MB storage
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDENTIFICATION METHOD:
OTHER INFORMATION: This sequence,
OTHER INFORMATION: corresponding to bovine basic fibroblast
OTHER INFORMATION: growth factor, can be found in Table 1,
OTHER INFORMATION: page 9, lines 9, 14, and 19, in the
OTHER INFORMATION: application, as filed.
PUBLICATION INFORMATION:
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                                                                                                          STREET: 805 Thir
CITY: New York
STATE: New York
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                           COUNTRY: USA
ZIP: 10022
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PUBLICATION DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAGES:
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Pred. No. 0.19;
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RESULT 11
US-08-231-894A-11
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Best Local Similarity 40.0
Matches 10; Conservative
                                                                                                                                                                                                                                 Sequence 11, Application US/08231894A
Patent No. 5851990
GENERAL INFORMATION:
APPLICANT: FUJISHIMA, AKIRA
APPLICANT: FUKUDA, TSUNEHIKO
TITLE OF INVENTION: BFGF MUTEIN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 07/806,771
FILING DATE: December 6, 1991
APPLICATION NUMBER: 07/17,506
FILING DATE: April 4, 1988
APPLICATION NUMBER: 07/062,925
FILING DATE: June 16, 1987
ATTORNEY/AGENT INFORMATION:
NAME: HOWARD M. Frankfort
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (212) 753-6237 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: & CUSHMAN
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                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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FILING DATE: January
APPLICATION NUMBER:
FILING DATE: June 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDENTIFICATION METHOD:
OTHER INFORMATION: This sequence,
OTHER INFORMATION: corresponding to bovine basic fibroblast
OTHER INFORMATION: growth factor, can be found in Table 1,
OTHER INFORMATION: page 9, lines 9, 14, and 19, in the
OTHER INFORMATION: application, as filed.
                                                                                                                          STREET: 130 I
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REFERENCE/DOCKET NUMBER: 5986/13586-US7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DESCRIPTION: Protein
COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                            STATE:
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                                                                                                                                             130 WATER STREET
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Wordperfect 5.1
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June 27, 1952
771
71991
                                    Diskette
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UMBER: 07/901,705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.1%; Score 60; DB 4; Length 145; 40.0%; Pred. No. 0.19; ive 5; Mismatches 10; Indels
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                                                                                                                                                                               BRONSTEIN, ROBERTS
                                                                                                                                                                                                                                     ITS PRODUCTION
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PRIOR APPLICATION DATA:

CURRENT APPLICATION DATA:

SOFTWARE:

FastSEQ Version 1.5

APPLICATION NUMBER: FILING DATE: 22-AP

22-APR-1994

US/08/231,894A

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 097655-1991
FILING DATE: 26-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 066381-1992
APPLICATION NUMBER: JP 066381-1992
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
NAME: RESNICK, DAVID S.

NAME: RESNICK, DAVID S.

1235
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                                                                                                                                                                                                                                                                                                                                                                        tent No. 5851110N:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULARY MOLECULARY NO ANTI-SENSE: NO ANTI-SENSE: NO Internal
                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,894A
FILING DATE: 22-APR-1994
                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                   APPLICANT: FUJISHIMA, AKIRA
APPLICANT: FUKUDA, TSUNEHIKO
TITLE OF INVENTION: BFGF MUTEIN AND ITS PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE: ORIGINAL SOURCE:
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REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                STATE: MACO
                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
APPLICATION NUMBER: US 07/873907 FILING DATE: 24-APR-1992
                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 YCKNGGFFLRIHPDGRVDGVREKSD 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
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TOPOLOGY: lir
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5851990
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                                                  22-APR-1994
N: 435
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US-08-231-894A-13
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; ORIGINAL SOURCE:
US-08-231-894A-12
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Best Local Similarity 40.0%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (617) 523-6440 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                               APPLICATION NUMBER: JP 0' FILING DATE: 26-APR-1991 PRIOR APPLICATION DATA:
                                                                                                                                             APPLICATION NUMBER: UFILING DATE: 22-APR-1 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                   SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: FUJISHIMA, AKIRA
APPLICANT: FUKUDA, TSUNEHIKO
TITLE OF INVENTION: BFGF MUTEIN AND ITS PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL:
                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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MOLECULE TYPE:
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APPLICATION NUMBER: JP 0
FILING DATE: 26-APR-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                APPLICATION NUMBER: US 07/873907 FILING DATE: 24-APR-1992 CLASSIFICATION: 435
APPLICATION NUMBER: JP 066381-1992 FILING DATE: 24-MAR-1992
                                                                                                                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                                      COMPUTER:
                                                                                                                                                                                                                                                                                                                       ZIP: 02109
                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                      CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                     STREET:
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REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: RESNICK, DAVID S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 WCTWDAFYLTVHPQGVIEGVRHLVD 27
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                                                                                                                                                                                                                                                                                                                                                                                     130 WATER STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146 amino acids
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24-MAR-1992
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                                                                 JP 097655-1991
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Pred. No. 0.19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
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; ORIGINAL SOURCE:
US-08-231-894A-13
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Best Local Similarity 40.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/08231894A Patent No. 5851990
                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/231,894A FILING DATE: 22-APR-1994 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/873907 FILING DATE: 24-APR-1992 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (617) 523-644
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
TELEFAX: (617) 523-6440 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: FUJISHIMA, AKIRA
APPLICANT: FUKUDA, TSUNEBIKO
TITLE OF INVENTION: BEGF MUTEIN AND ITS PRODUCTION
                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 097655-1991
FILING DATE: Z6-APR-1991
PRIOR APPLICATION DATA:
APPLICATION UMBER: JP 066381-1992
FILING DATE: Z4-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
                                TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: MACO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS ADDRESSEE: & CUSHMAN STREET: 130 WATER STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 YCKNGGFFLRIHPDGRVDGVREKSD 48
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STRANDEDNESS: sir
TOPOLOGY: linear
                                                                REFERENCE/DOCKET NUMBER:
                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: RESNICK, DAVID
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                                                                                              DAVID S
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0.19;
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US-08-231-894A-15
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                                                                                                                                        TELEFAX: (617) 523-64
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 097655-1991
FILING DATE: 26-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 066381-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                  APPLICATION NUMBER: JP 066381-1992
FILING DATE: 24-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                            MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                           SEQUENCE CHARACTERISTICS:
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APPLICANT: FUKUDA, TSUNEHIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
RAGMENT TYPE:
                INTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 24-APPLICATION: 43
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: si
TOPOLOGY: linear
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                                                             TOPOLOGY:
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                                                                            STRANDEDNESS:
                                                                                                                                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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Local Similarity 40.0%;
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24-APR-1992
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ID NO: 15:
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Maximum
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Listing first 45 summaries
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1 FGWCTWDAFYLTVH
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Gapop 10.0 , Gapext 0.5
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2: /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:
3: /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:
4: /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:
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                                                                                                                                                   SUMMARIES
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No E	Score	Match	Match Length DB	BG	ID	Description
1	181	100.0		19	AAW53567	Cucumber raffinose
N	181	100.0		20	AAY17422	Cucumber raffinose
ω	181	100.0		19	AAW53570	Cucumber raffinose
4	181	100.0		20	AAY17417	Cucumber raffinose
Ç	158	87.3		21	AAY70978	Soybean raffinose
σ	148	81.8		19	AAW57886	Broad bean raffino
7	148	81.8		20	AAY30142	Amino acid sequenc
8	146	80.7	587	19	AAW57888	Japanese artichoke
9	146	80.7		20	AAY30144	Amino acid sequenc
10	146	80.7		22	AAB98659	Soybean protein: S

The present sequence is a cucumber raffinose synthase fragment.

Claim 2; Page 16; 26pp; Japanese.

11122222222222222222222222222222222222	11 12 13 14 15
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33333333333333333333333333333333333333	
751 751 753 753 7563 7563 770 807 746 100 150 140 443 443 444 445 445 445 445 1101 1101 1101 1101	781 781 781 777 777 783
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ALIGNMENTS

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RESULT 1
AAW53567
Raffinose synthase gene - transformed plant
                                      WPI; 1998-264858/24.
                                                                             26-JUL-1996;
26-APR-1996;
                                                                                                          28-APR-1997;
                                                                                                                               07-APR-1998
                                                                                                                                                  JP10084973-A.
                                                                                                                                                                      Cucumis sativus.
                                                                                                                                                                                         Cucumber; raffinose synthase; sucrose; galactinol
                                                                                                                                                                                                            Cucumber raffinose synthase residues 215 to 244.
                                                                                                                                                                                                                                06-JUL-1998 (first entry)
                                                                                                                                                                                                                                                    AAW53567;
                                                                                                                                                                                                                                                                       AAW53567 standard; peptide; 30 AA.
                                                         (AJIN ) AJINOMOTO KK.
                                                                             96JP-0198079
96JP-0107682
                                                                                                          97JP-0111124
                 useful for preparation of raffinose in
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RESULT 2
AAX17422
ID AAX1
XX AAX1
AC AAX1
XX Cucu
XX Raff
XX Raff
XX JP11
XX JP11
XX AFF
CC UCU
XX AFF
CC The
CC Gene
CC raff
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XX Sequ
                                                                        RESULT 3
AAW53570
 DXXXX
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Matches 30
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Best Local (
                                                                                                                                                                                              Matches
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 06-JUL-1998
                             AAW53570;
                                                            AAW53570 standard;
                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                              of forming raffinose from sucrose and galactinol. The raffinose synthass gene can be used for expression in a plant for the production of raffinose. The raffinose synthase can give raffinose from sucrose and galactinol efficiently. The present sequence represents a raffinose
                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Page 21; 37pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                    New raffinose synthase gene - for production of raffinose sucrose and galactinol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-340516/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cucumber raffinose synthase peptide SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 30; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention describes a raffinose synthase, having an forming raffinose from sucrose and galactinol. The raffinose
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                                                                                                                                     FGWCTWDAFYLTVHPQGVIEGVRHLVDGGC
                                                                                                                                                                                              30;
                                                                                                                                                                                                                                                                                    peptide from cucumber.
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ilarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97JP-0292969
                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sucrose; galactinol
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Pred. No. 2.5
9; Mismatches
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-19;
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                                                                                                                                                                                                                                                                                                                                                           an activity
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                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                               synthase
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RESULT 4
AAY17417
ID AAY1
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is cucumber raffinose synthase, which forms raffinose from sucrose and galactinol, has an optimum pH of 6 to 8 and working temperature of 35 to 40 degrees C, has a molecular weight of 75 to 95 kDa by gel filtration or 90 to 100 kDa by PAGE and SDS-PAGE under reductive conditions and is inhibited by iodoacetamide, N-ethylmaleimide and myoinositol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-264858/24.
N-PSDB; AAV22250.
New raffinose synthase sucrose and galactinol
                                                                                                                                                                                                                                   Cucumber raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Pages 17-20; 26pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Raffinose synthase gene - useful for preparation of raffinose transformed plant % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JP10084973-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cucumis sativus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cucumber; raffinose synthase; sucrose; galactinol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cucumber raffinose synthase.
                                   N-PSDB; AAX61238.
                                                                                                                  24-OCT-1997;
                                                                                                                                                               JP11123080-A.
                                                                                                                                                                                     Cucumis sativus
                                                                                                                                                                                                          Raffinose synthase; sucrose; galactinol
                                                                                                                                                                                                                                                        29-JUL-1999
                                                                                                                                                                                                                                                                               AAY17417;
                                                                                                                                                                                                                                                                                                      AAY17417 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AJIN ) AJINOMOTO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUL-1996;
26-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-APR-1997;
          New raffinose
                                               WPI; 1999-340516/29.
                                                                    (AJIN ) AJINOMOTO KK
                                                                                                                                         11-MAY-1999
                                                                                                                                                                                                                                                                                                                                                               215
                                                                                                                                                                                                                                                                                                                                                                         FGWCTWDAFYLTVHPQGVIEGVRHLVDGGC
                                                                                                                                                                                                                                                                                                                                                               FGWCTWDAFYLTVHPQGVIEGVRHLVDGGC
                                                                                                                                                                                                                                                                                                                                                                                                            1 Similarity 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                          784 AA;
                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                        (first entry)
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96JP-0107682
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                                                                                             97JP-0292969
                                                                                                                  97JP-0292969
                                                                                                                                                                                                                                   synthase
                                                                                                                                                                                                                                                                                                      Protein;
            gene
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                                                                                                                                                                                                                                                                                                      784
                                                                                                                                                                                                                                                                                                                                                                                                           Score 181; DB 19;
Pred. No. 1.2e-17;
; Mismatches 0;
            for production
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                                                                                                                                                                                                                                                                                                                                                                244
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             of raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 784;
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                              Query Match
Best Local Similarity
Matches 26; Conserv
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Best Local Similarity
Matches 30; Conserv
                                                                                      The present sequence is a raffinose synthase from clone sfil.pk125.d4 isolated from a soybean immature flower cDNA library sfil. Raffinose synthase is involved in the biosynthesis of raffinose and higher homologues in the raffinose saccharide family from sucrose. The present sequence is useful for reducing the raffinose saccharide content of soybean seeds which improves the nutritional quality of the soy protein products derived from them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a raffinose synthase, having an of forming raffinose from sucrose and galactinol. The raffinose gene can be used for expression in a plant for the production of raffinose. The raffinose synthase can give raffinose from sucros and galactinol efficiently. The present sequence represents raffined galactinol efficiently.
                                                                     Sequence
                                                                                                                                                                      Claim 2;
                                                                                                                                                                                      Nucleic acids and encoded proteins involved in the biosynthesis raffinose, useful for producing soybean seeds with a reduced racontent and therefore improved nutritional quality -
                                                                                                                                                                                                                                                             Allen
                                                                                                                                                                                                                                                                                                                                          04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                             WO200024915-A2
                                                                                                                                                                                                                                                                                                                                                                                 Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                   Soybean; raffinose synthase; raffinose saccharide; clone sfll.pk125.d4; nutritional; soy protein.
                                                                                                                                                                                                                                                                                                                                                                                                                              Soybean raffinose synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY70978 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           synthase from cucumber.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2;
                                                                                                                                                                                                                                                                                nd ( odnd)
                                                                                                                                                                                                                                                                                                   23-OCT-1998;
                                                                                                                                                                                                                                                                                                                       22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FGWCTWDAFYLTVHPQGVIEGVRHLVDGGC 30
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FGWCTWDAFYLTVHPQGVIEGVRHLVDGGC
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                                                                                                                                                                                                                                                             SM,
                                                                                                                                                                                                                                AAD00335
                                                                                                                                                                    Page 47-49; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 25-27; 37pp; Japanese
                                                                                                                                                                                                                                                             Hitz WD;
                                                                                                                                                                                                                                                                                PONT DE NEMOURS
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                                                                     758 AA;
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ilarity 100.0%;
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                               Conservative
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                                       87.3%;
86.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                from clone sfll.pk125.d4.
                              Score 158; DB Pred. No. 2.6e 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          758
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Pred. No. 1.2
D; Mismatches
                                                                                                                                                                                                                                                                                 (Ŧ)
                                       DB 21;
.6e-14;
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..2e-17;
                                               Length 758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    represents raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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                                                                                                                                                                                                  raffinose
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                             Gaps
                                                                                                                                                                                                            of
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ARESULT 7
ARAY30142
ID ARY3
XX ARY3
AC ARY3
AC ARY3
AC ARY3
XX Vici
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents the broad bean raffinose synthetase of the invention. The raffinose synthetase is capable of producing raffinose by combining a D-galactosyl group through an alpha (1-6) bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule. The DNA can be used to modify metabolism of a host organism by introducing into the host organism or its cell so that the content of the raffinose family oligosaccharides in the host organism or cell is changed. Raffinose oligosaccharides are useful as food additives with beneficial effects on the gastrointestinal flora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW57886 standard;
                                     Raffinose synthase; plant; broad bean; sucrose; raffinose.
                                                                                                                                                                     AAY30142;
                                                                                                                                                                                                            AAY30142 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid molecule encoding plant raffinose synthetase capable of producing raffinose, used as food additives with beneficial effects on gastrointestinal flora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Raffinose synthetase; metabolism modification; food additive; gastrointestinal flora; broad bean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Broad bean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW57886;
                                                                                   Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 - JUN - 1998
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                                                                                                                                                                                                                                                                                                                    238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202 FGWCTWDAFYLTVHPEGVREGVKGLVDGGC
                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                         1 FGWCTWDAFYLTVHPQGVIEGVRHLVDGGC
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                                                                                                                                                                                                                                                                                                                    FGWCTWDAFYLKVHPKGVWEGVKSLTDGGC
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                                                                                                                                                                                                                                                                                                                                                                                                       24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 26-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wantanabe
                                                                                 sequence of a raffinose synthase protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       799 AA;
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                           (first entry)
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                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                    81.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                   2
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 148; DB 19;
Pred. No. 8.1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                             19;
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RESULT 8
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Best Local S
Matches 24
                         This sequence
                                                                          Claim 1; Page 36-38; 44pp;
                                                                                                                      New nucleic acid molecule encoding plant raffinose synthetase capable of producing raffinose, used as food additives with beneficial effects on gastrointestinal flora
                                                                                                                                                                                                                                                                                                      0eda
                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stachys sieboldii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gastrointestinal flora; Japanese artichoke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Japanese artichoke raffinose synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a raffinose synthase protein. The sequence is isolated from plant material of broad beans. The protein forms raffinose by complexing alpha(1 to 6) - D-galactosyl hydroxyl group of the 6C of D-glucose residue in sucrose molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New raffinose synthase gene - is prepared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAZ10001.
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18-DEC-1996;
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                                                                                                                                                                                                                             N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                       (SUMO)
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                                                                                                                                                                                                                                                                                                      K, Wantanabe E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FGWCTWDAFYLKVHPKGVWEGVKSLTDGGC 267
                                                                                                                                                                                                                                                                                                                                                       SUMITOMO CHEM
                                                                                                                                                                                                                             AAV40802.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       799 AA;
     The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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is the Japanese artichoke raffinose e raffinose synthetase is capable of
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96JP-0338673.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81.8%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                       CO LTD
                                                                             English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 148; DB Pred. No. 8.1e 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 20;
1.1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plant material
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 799;
synthetase producing r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
  e of the
raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
     γd
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RESULT 10 AAB98659

ID

AAB98659 standard;

protein;

XX AC

AAB98659;

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RESULT 9
AAY30144
ID AAY3
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                                                    δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                           Matches
                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       combining a D-galactosyl group through an alpha (1-6) bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule. The DNA can be used to modify metabolism of a host organism by introducing into the host organism or its cell so that the content of the raffinose family oligosaccharides in the host organism or cell is changed. Raffinose oligosaccharides are useful as food additives with beneficial effects on the gastrointestinal flora.
                                                                                                                                                                                                                                                                           The present sequence represents a raffinose synthase protein. The sequence is isolated from plant material. The protein forms raffinose by complexing alpha(1 to 6). D-galactosyl hydroxyl group of the 6C of D-glucose residue in sucrose molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-511112/43.
N-PSDB; AAZ10003.
                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stachys sieboldii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Raffinose synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY30144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY30144 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New raffinose synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-NOV-1997;
18-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JP11215984-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-OCT-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SUMO ) SUMITOMO CHEM CO LTD
  107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FGWCTWDAFYLTVHPQGVIEGVRHLVDGGC 30
                                                    1 FGWCTWDAFYLTVHPQGVIEGVRHLVDGGC 30
FGWCTWDAFYLNVQPHGVMEGVQGLVDGGC 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FGWCTWDAFYLNVQPHGVMEGVQGLVDGGC 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24;
                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       Page 30-31; 40pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           587 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                              Conservative
                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97JP-0329006.
96JP-0338673.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97JP-0342899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plant; sucrose;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of a raffinose synthase protein.
                                                                                                                                        80.7%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene - is prepared from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
                                                                                                                                        Score 146; DB 20;
Pred. No. 1.1e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 146; DB 19;
Pred. No. 1.1e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plant material
                                                                                                                                                                     Length 587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       587;
                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                 Gaps
                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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В
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Best Local S
Matches 24
                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a mutant protein of raffinose synthase in which at least one aromatic amino acid present at the position of about 1-7 amino acids from the N-terminus is deleted or replaced. The mutant protein can be used for reducing the raffinose oligosaccharide content in a plant body. The present protein from soybean, was used in the present inventory in the present protein from soybean.
WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycine
                   Oeda
                                    (SUMO)
                                                        18-DEC-1996;
                                                                          18-DEC-1997;
                                                                                             24-JUN-1998
                                                                                                              EP849359-A2
                                                                                                                                 Glycine
                                                                                                                                                  Raffinose synthetase; metabolism modification; gastrointestinal flora; soybean.
                                                                                                                                                                                Soybean
                                                                                                                                                                                                   23-SEP-1998
                                                                                                                                                                                                                      AAW57887;
                                                                                                                                                                                                                                        AAW57887 standard; Protein; 781 AA
                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 18-20; 30pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel mutant protein of raffinose synthase is useful for raffinose oligosaccharide content in a plant body -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JUL-2000; 2000JP-0200571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JP2001078783-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SUMO)
                                                                                                                                                                                                                                                                                    present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-313373/33.
                                                                                                                                 max.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           max
                                                                                                                                                                                raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMITOMO CHEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutein;
                                     SUMITOMO CHEM CO LTD
                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein:
                   Wantanabe E;
                                                                                                                                                                                                                                                                                                                                                                 780
                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first
                                                                                                                                                                                                                                                                                                                                                                 Ą,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99JP-0196036
                                                        96JP-0338673.
                                                                          97EP-0122417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      raffinose synthase;
                                                                                                                                                                                synthetase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                   80.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ID 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ဗ
                                                                                                                                                                                                                                                                                                                          Score 146; DB
Pred. No. 1.5e
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      raffinose oligosaccharide reduction;
                                                                                                                                                                                                                                                                                                                                    DB 22;
.5e-12;
                                                                                                                                                             food additive;
                                                                                                                                                                                                                                                                                                                                            Length 780;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reducing
                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                          Gaps
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RESULT 12
AAY30143
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 Query Match
Best Local S
Matches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents the soybean raffinose synthetase of the invention. The raffinose synthetase is capable of producing raffinose by combining a D-galactosyl group through an alpha (1-6) bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule. The DNA can be used to modify metabolism of a host organism by introducing into the host organism or its cell so that the content of the raffinose family oligosaccharides are useful as food additives with beneficial effects on the gastrointestinal flora.
                                                                         The present sequence represents a raffinose synthase protein. The sequence is isolated from plant material. The protein forms raff by complexing alpha(1 to 6) - D-galactosyl hydroxyl group of the of D-glucose residue in sucrose molecules.
                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 31-34; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid molecule encoding plant raffinose synthetase capable of producing raffinose, used as food additives with beneficial effects on gastrointestinal flora
                                                                                                                                      Claim 8;
                                                                                                                                                              New raffinose synthase gene -
                                                                                                                                                                                          N-PSDB; AAZ10002
                                                                                                                                                                                                    WPI; 1999-511112/43.
                                                                                                                                                                                                                                                    28-NOV-1997;
18-DEC-1996;
                                                                                                                                                                                                                                                                                          12-DEC-1997;
                                                                                                                                                                                                                                                                                                                                           JP11215984-A
                                                                                                                                                                                                                                                                                                                                                                    Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                          Raffinose synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of a raffinose synthase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                               26-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY30143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY30143 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAV40801
                                                                                                                                                                                                                            (SUMO ) SUMITOMO CHEM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         220 FGWCTWDAFYLKVHPSGVWEGVKGLVEGGC 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FGWCTWDAFYLTVHPQGVIEGVRHLVDGGC
 Similarity
24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                     Page 25-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              781 AA;
                                                   781 AA;
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                    97JP-0329006
96JP-0338673
                                                                                                                                                                                                                                                                                          97JP-0342899
                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                           plant;
                                                                                                                                    40pp;
             80.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80.7%;
                                                                                                                                     Japanese
Score 146; DB
Pred. No. 1.5e
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           sucrose;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 146; DB 19;
Pred. No. 1.5e-12;
                                                                                                                                                              is prepared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30
             DB 20;
                                                                                                                                                              from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                              ø
                       Length 781;
                                                                                                                                                             plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 781;
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
 0
                                                                                     rattinose
the 6C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         raffinose by
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 Gaps
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1 FGWCTWDAFYLTVHPQGVIEGVRHLVDGGC 30

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RESULT 14
AAY32075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                Matches
               Location/Qualifiers
                                                                                                                                                                                                                                The the
       Misc-difference
                                          Brassica napus
                                                       Raffinose synthase;
                                                                      Rapeseed raffinose synthase.
                                                                                     17-JAN-2000
                                                                                                   AAY32075;
                                                                                                                 AAY32075 standard; Protein;
                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                    Example 6; Page 24-27; 36pp; English
                                                                                                                                                                                                                                                                 New soybean plant promoters useful for generating transgenic plants with desired properties
                                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                              WPI; 2001-104537/12.
                                                                                                                                                                                                                                                                                                            Ishige F,
                                                                                                                                                                                                                                                                                                                         (SUMO ) SUMITOMO CHEM CO LTD.
                                                                                                                                                                                                                                                                                                                                        30-APR-1999;
01-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                             27-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                           02-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                         EP1048733-A2
                                                                                                                                                                                                                                                                                                                                                                                                      Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                                                    Plant promoter; transgenic plant; desired property.
                                                                                                                                                                                                                                                                                                                                                                                                                                Soybean raffinose synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                               07-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB49400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB49400 standard; Protein;
                                                                                                                                                     220 FGWCTWDAFYLKVHPSGVWEGVKGLVEGGC 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              220
                                                                                                                                                           1 FGWCTWDAFYLTVHPQGVIEGVRHLVDGGC 30
                                                                                                                                                                                                                              present invention provides novel plant promoters which can be used production of transgenic plants which express genes with desired % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                            781 AA;
                                                                                                                                                                                                                                                                                                            Watanabe E,
                                                                                                                                                                                Conservative
                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                             2000EP-0108962
                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                        99JP-0124527.
99JP-0247211.
/note=
              /note= "encoded by GGY"
                                                       rapeseed; transgenic plant.
                                                                                                                                                                                      80.7%;
"encoded by GGW"
                                                                                                                                                                                                                                                                                                            Oeda K;
                                                                                                                  572
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                                                                                                                                                                               Score 146; DE
Pred. No. 1.5e
2; Mismatches
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..5e-12;
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30-APR-1998;
04-DEC-1998;
10-DEC-1998;
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Misc-difference 144
       Misc-difference
                            Brassica
                                                        Mustard raffinose synthase.
                                                                       17-JAN-2000
                                                                                     AAY32074;
                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
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                                                                                                                                                                  L Similarity
24; Conserv
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                           juncea
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                                                                      (first entry)
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148
/note=
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                                                                                                                                                                        79.6%;
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(see AAZ20210) encoding the enzyme was isolated from rapessed cv. Westar leaf cDNA by PCR. Probes or primers generated from plant raffinose synthase genes (see AAZ20207-10) may be used to obtain other raffinose synthase genes by labeled detection or amplification (claimed). These genes may be used to control the levels of raffinose produced in plants. Antisense genes can be used to knock out existing gene activity, and sense genes can be used to knock of gene activity. The resulting transgenic plants may be used as a food source to alter the growing conditions for gut enterobacteria, providing general health advantages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents rapessed raffinose synthase, a protein that can bind a D-galactosyl group through an alpha(1-6) bond to the hydroxy group attached to the carbon atom at the 6-position of the D-glucose residue in a sucrose molecule to form raffinose. cDNA
                                                                                                                                                 Raffinose synthase; mustard; transgenic plant
                                                                                                                                                                                                                                                                                                                                                                   AAY32074 standard; Protein; 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 27; Page 36-38; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New sense and antisense genes, useful for altering the level raffinose in food plants - \,
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98JP-0120551.
98JP-0345590.
98JP-0351246.
                  Location/Qualifiers 210
"encoded by ACR"
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Search completed: March 27, 2003, 10:03:41 Job time: 22.2195 secs
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Matches 24; Conserv
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30-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-593144/51.
N-PSDB; AAZ20209.
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                                                                                                                              777 AA;
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H64744	S55456	AF0242	S39592	AC3600	A95228	E98092	T23250	AB0521	AD0533	F71427	AD0798	S52809	S52799	ERAD31	AF2067
yaeD protein - Esc	GAM1 protein - Pla	probable exported	prolyl aminopeptid	cellulase (EC 3.2.	bacteriocin format	cylM protein, cyto	hypothetical prote	AmpE protein (impo	conserved hypothet	hypothetical prote	probable phosphata	hypothetical prote	hypothetical prote	early E3A 12.1K pr	histidinol phospha

ALIGNMENTS

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probable seed inhibition protein - chickpea (fragment)
C;Species: Cicer arietinum (chickpea, garbanzo)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
C;Accession: T09530
R;Cervantes, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable imbibition protein - wild cabbage
C;Species: Brassica oleracea (wild cabbage)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997
C;Accession: S45033
R;Fujikura, Y; Karssen, C.K.
submitted to the EMBL Data Library, May 1994
A;Description: Cauliflower CDNA encoding a putative imbibition protein.
A;Reference number: S45033
A;Accession: S45033
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S45033
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                                                                                                                                          C;Genetics:
A;Gene: sip
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A;Molecule type: mRNA
A;Residues: 1-357 <CER>
A;Cross-references: EMBL:X95875; NID:g1212811
                                                                                                                                                                                                                                                                 A; Reference number: A; Accession: T09530
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A; Residues: 1-765 < FUJ>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 19; Conserv
31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FGWCTWDAFYLTVHPQGVIEGVRHLVDGG 29
                  FGWCTWDAFYLTVHPQGVIEGVRHLVDGG
FGWCTWDAFYTDVTAEGVEEGLKSLSEGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61.3%;
                                                                                     59.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 111; DB Pred. No. 2.3e 3; Mismatches
                                                                                     Score 108;
Pred. No. 2
                                                                                                                                                                             seed
                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.3e-07;
7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 765;
                                                                                                      Length 357;
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                                                                      Indels
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                                                                      0
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A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana A;Reference number: A85001; MUID:20083488; PMID:10617198 A;Accession: C85025
                                                                                                                                                                                                         hypothetical protein AT4g01970 [imported] - Arabidopsis thaliana (:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001 C:Accession: C85025
                    A;Cross-references: GB:NC_001268; NID:g7268581; PIDN:CAB80690.1; GSPDB:GN00140
                                           A; Molecule type: DNA
A; Residues: 1-807 <STO>
                                                                                   A;Status: preliminary
                                                                                                                                                                R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprir Nature 402, 769-777, 1999
                                                                                                                                                                                                       C; Accession:
                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                          δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-773 <BEN>
A; Cross-references: EMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       imbibition protein homolog - Arabidopsis thaliana
N;Alternate names: protein T8H10.120
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sip1
C;Spe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: Z23014
A; Accession: T46188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: R;Benes, V.;
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A; Residues: 1-757 <HEC>
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C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Sep-1997
C;Accession: S27762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: cultivar Columbia; BAC clone T8H10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the Protein
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        Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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    barley

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146/1; 176/2; 192/3; 223/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence Database,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.7%;
62.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ho, T.H.
Library, February 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    259/2;
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5.9e-07;
hes 8;
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QΥ
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RESULT 7
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                                                                            A; Introns: 5/2; 25/3; A; Note: A_IG002N01.5
                                                                                                                                         A: Experimental source: cultivar Columbia C: Genetics:
                                                                                                                                                                                                                                                                                                                                                      hypothetical protein A_IG002N01.5 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Decies: Arabidopsis thaliana (mouse-ear cress) C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 24-Mar-1999 C;Accession: T01717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
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C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                  A; Map position: 4
                                                                                                                                                                           A;Cross-references: EMBL:AF007269; NID:g2191126; PID:g2191156
                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-371 <SCH>
                                                                                                                                                                                                                                   A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                       A; Reference number: A; Accession: T01717
                                                                                                                                                                                                                                                                            A;Description: The sequence A;Reference number: 214407
                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, June 1997 A; Description: The sequence of A. thaliana IG002N01
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A;Molecule type: DNA
A;Residues: 1-1170 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A86141; A; Accession: C96599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Theologis, A.; Ecker, J.R.; Palm, Chin, C.W.; Chung, M.K.; Conn, L.;
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                                      Query Match
    Matches
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Best Local
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    Local Similarity
les 11; Conser
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                                                                                                                                                                                                                                                                                                                                  P.; Maggi, L
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    Conservative
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                                                                                              103/3; 126/1; 174/2;
                      39.8%;
84.6%;
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51.9%;
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62.1%;
    0;
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Pred. No. 0.00
3; Mismatches
                                      Score 72;
                      Pred. No. 0.029;
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Pred. No. 1
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Conway, A.B.; Conway, A.
Mismatches
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                                                                                                240/1;
                                        DB 2;
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.2e-06;
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                                                                                              284/1; 295/1;
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  2;
                                    Length 371;
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  Indels
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                                                                                                333/2;
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Maiti, R.; Marzia
  Gaps
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FGWCTWDAFYLTV

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RESULT 10
S00185
                    A;Title: Primary structure of ovine pituitary basic fibroblast growth factor A;Reference number: S00185; MUID:88055577; PMID:3678486 A;Accession: S00185
                                                                                                                                                                         basic fibroblast growth factor - sheep N;Alternate names: prostatropin C;Species: Ovis orientalis aries, Ovis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Winkles, J.A.; Friesel, R.; Alberts, G.F.; Janat, M.F.; Liau, Am. J. Pathol. 143, 518-527, 1993
A;Title: Elevated expression of basic fibroblast growth factor A;Reference number: 146711; MUID:93343209; PMID:8342599
A;Accession: 146711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fibroblast growth factor - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 16-Jul-1999
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Nature 406, 477-483, 2000
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C;Species: Vibrio cholerae
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                                                                                      R;Simpson, R.J.; Moritz, R.L.; Lloyd, C.J.; Fabri, L.J.; Nice, E.C.; Rubira, M.R.; FEBS Lett. 224, 128-132, 1987
                                                                                                                                  C;Date: 10-Sep-1999 #sequence_revision C;Accession: S00185
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A;Experimental source: serogroup O1; strain N16961; biotype El Tor
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  A; Molecule type:
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;Accession: E82168
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                      A; Title: Isolation of cDNAs encoding four mouse FGF family members A; Reference number: A37360; MUID:90201563; PMID:2318343 A; Accession: C37360
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                                                                                    R; Hebert, J.M.; Basilico, C.;
Dev. Biol. 138, 454-463, 1990
A;Status: preliminary
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A:Cross-references: EMBL:X07285; NID:g56203; PIDN:CAA30265.1; R;El-Husseini, A.E.D.; Paterson, J.A.; Myal, Y.; Shiu, R.P.C. Biochim. Biophys. Acta 1131, 314-316, 1992
A;Title: PCR detection of the rat brain basic fibroblast growt A;Reference number: $24309; MUID:92329546; PMID:1378302
A;Accession: $24309
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A;Title: Nucleotide sequence of rat basic fibroblast growth fa;Reference number: S00876; MUID:88262516; PMID:3387229
A;Accession: S00876
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N;Alternate names: bFGF
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 16-Jul-1999
C;Species: Mus musculus (house mouse)
C;Date: 17-Apr-1993 #sequence_revision
C;Accession: C37360
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A;Molecule type: mRNA
A;Residues: 35-154 <ELH>
A;Cross_references: EMBL:X61697; NID:g56143; PIDN:CAA43863.1;
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A;Title: Complementary DNA cloning and sequencing of rat ovarian basic fibrol A;Reference number: A31674; MUID:89061721; PMID:3196337
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C; Superfamily: fibroblast growth factor
                                                                       basic fibroblast growth factor -
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A; Residues: 1-154 < KUR>
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A; Residues: 1-154 <SHI>
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A;Molecule type: protein
A;Residues: 16-35 <BER>
A;Residues: 16-35 <BER>
R;Ueno, N.; Baird, A.; Esch, F.; Ling, N.; Guillemin, R.
Mol. Cell. Endocrinol. 49, 189-194, 1987
Mol. Cell. Endocrinol. 49, 189-194, 1987
A;Title: Isolation and partial characterization of basic fibroblast growth factor from A;Reference number: A61551; MUID:87162856; PMID:3556754
A;Accession: A61551
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A;Residues: 3-157 <AB2>
A;Residues: 3-157 <AB2>
R;Milner, P.G.; Li, Y.S.; Hoffman, R.M.; Kodner, C.M.; Siegel, N.R.; Deuel,
R;Milner, Biophys. Res. Commun. 165, 1096-1103, 1989
A;Title: A novel 17 kD heparin-binding growth factor (HBGF-8) in bovine utel
A;Reference number: A33784; MUID:90121211; PMID:2610682
A;Accession: A33784
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R;Abraham, J.A.; Whang, J.L.; Tumolo, A.; Mergia, A.; Fiddes, J.C.
Cold Spring Harb. Symp. Quant. Biol. 51, 657-668, 1986
Cold Spring Harb. Symp. Quant Biol. 51, 657-668, 1986
A;Title: Human basic fibroblast growth factor: nucleotide sequence,
A;Reference number: A90924; MUID:87217066; PMID:3472745
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C;Date: 13-Aug-1986 #sequence_revision 02-Jun-1995 #text_change 24-Nov-1999
C;Accession: A24663; A32878; A33784; A61550; A61551; A60310; A61094; A01386; ¿R;Abraham, J.A.; Mergia, A.; Whang, J.L.; Tumolo, A.; Friedman, J.; Hjerrild, Science 233, 545-548, 1986
                                                                                                                                                                                                                                A; Reference number: A60310; A; Accession: A60310
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A; Residues: 1-154 <HEB>
A; Cross-references: GB: M30644; NID:g193296;
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A; Residues: 23-35,'X',37-42 <UEN>
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A; Residues: 27-35, 'X', 37-41 <UE3>
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A; Residues: 3-157 < ABR>
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N;Alternate names: bFGF; kidney-derived growth factor; prost
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1.; Baird, A.; Esch, F.; Snimasen., -...

apt. 16, 135-145, 1986

Purification and partial characterization of a mitogenic factor purification and partial characterization of a mitogenic factor pumber: A60310; MUID:87119165; PMID:3809608
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C; Superfamily: fibroblast growth factor: hep

F; 1-157/Product: basic fibroblast growth factor, blocked amino end; growth factor; hep

F; 1-157/Product: basic fibroblast growth factor, pituitary gamma form #status experim

F; 12-157/Product: basic fibroblast growth factor, pituitary alpha form #status experi

F; 16-157/Product: basic fibroblast growth factor, pituitary short form #status predic

F; 16-157/Product: basic fibroblast growth factor, pituitary short form #status predic

F; 27-157/Product: basic fibroblast growth factor, hepatic form #status experimental 

F; 27-157/Product: basic fibroblast growth factor, renal form #status experimental 

F; 27-33,118-121/Region: heparin binding #status predicted

F; 4/Modified site: blocked amino end (Ala) (in mature form pituitary gamma) (probably
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A; Title: Primary structure of bovine pituitary basic fibroblast growth factor (FGF) a A; Reference number: A01386; MUID:86016731; PMID:3863109
A; Accession: A01386
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A; Molecule type: protein
A; Residues: 12-26 <BOH>
A; Residues: 12-26 <BOH>
C; Comment: The acidic and basic fibroblast growth factors are the major endothelial-c
ell types in vitro (although bFGF is 30-100 times more potent than aFGF in stimulatin
C; Comment: This protein binds heparin more strongly than does aFGF.
A; Cross-references: GB: J04513; NID: g183083; R; Shibata, F.; Baird, A.; Florkiewicz, R.Z.
                                                                                                    A; Residues: 1-210 < PRA>
                                                                                                                                                      A; Molecule type: mRNA
                                                                                                                                                                                                        A;Reference number: A32398;
A;Accession: A32398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    basic fibroblast growth factor precursor, 22.5K form - human N;Alternate names: bFGF; fibroblast growth factor 2; prostat N;Contains: basic fibroblast growth factor, 18K form
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A;Title: Isolation and partial molecular characterization of F
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A;Molecule type: protein
A;Residues: 27-35', X', 37-43 <BAI>
A;Experimental source: kidney
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A;Title: Isolation and partial characterization of an en
A;Reference number: A60316; MUID:86095426; PMID:4081126
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A;Title: Isolation of fibroblast growth factor from bovine a A;Reference number: A61094; MUID:86081530; PMID:3940857
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A;Accession: ....
A;Accession: type: mRNA
A;Residues: 56-210 <ABR>
A;Residues: 56-210 <ABR>
A;Note: the authors translated the codon GAA for residue 108 as
A;Note: the authors translated the codon GAA for residue 108 as
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A;Residues: 56-210 <KUD>
A;Residues: 56-210 <KUD>
A;Residues: 56-210 <KUD>
A;Cross-references: GB:M27968; NID:g182562; PIDN:ANA52448.1; PID:g18
A;Cross-references: GB:M27968; NID:g182562; PIDN:ANA52448.1; PID:g18
Cold Spring Harb. Symp. Quant. Biol. 51, 657-668, 1986
Cold Spring Harb. Symp. Quant. Biol. 51, 657-668, 1986
A;Title: Human basic fibroblast growth factor: nucleotide sequence,
A;Reference number: A90924; MUID:87217066; PMID:3472745
A;Accession: B32878
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A;Title: Amino-terminal sequence of a large form of basic fibrobl A;Reference number: A25824; MUID:87156686; PMID:2435284
A;Accession: A25824
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A; Residues: 'XX', 86-88,'X', 90-91,'X', 93-95 <SH3>
A; Residues: 'XX' 86-88, 'X', 90-91,'X', 93-95 <SH3>
A; Residues: 'XX', 86-88, 'X', 90-91,'X', 93-95 <SH3>
A; Residues: C-Li21 hepatocellular carcinoma cell
A; Note: sequence extracted from NCBI backbone (NCBIP:71595)
A; Accession: B54316
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A;Residues: 1-155 <AB2>
A;Residues: 1-155 <AB2
A;Residues: 1-155
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A;Title: Human basic fibroblast growth factor: nucleotide A;Reference number: S00297; MUID:87053817; PMID:3780670
A;Accession: S00297
                                           FEBS
                                                                                                                    A;Molecule type: protein
A;Residues: 65-102,'X',104-105 <GIM>
A;Experimental source: brain
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A; Residues: 'XXX', 19, 'X', 21-29 <SH2>
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                                      , P.; Frater-Schroder, M.; Bohlen,
204, 203-207, 1986
characterization
of endothelial cell mitogens
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A; Residues: 95-182 <RES>
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A; Molecule type: mRNA
A; Residues: 54-210 <SOM>
A; Residues: 54-210 <SOM>
A; Cross-references: EMBL.M17599; NID:9183086; PIDN:AAA52534.1; PID:9183087
A; Pantoliano, M.W.; Horlick, R.A.; Springer, B.A.; Van Dyk, D.E.; Tobery, 'Blochemistry 33, 10229-10248, 1994
Blochemistry 33, 10229-10248, 1994
A; Title: Multivalent ligand-receptor binding interactions in the fibroblas: A; Reference number: A55784; MUID:94347757; PMID:7520751
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A;Accession: B24301
A;Molecule type: protein
A;Residues: 65-88,'X',90-98,'X',100 <GAU>
R;Sommer, A.; Brewer, M.T.; Thompson, R.C.; Moscatelli, D.; P
Blochem. Biophys. Res. Commun. 144, 543-550, 1987
A;Title: A form of human basic fibroblast growth factor with
A;Reference number: S42242; MUID:87213238; PMID:3579930
A;Accession: S42242
A;Status: preliminary
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C;Superfamily: fibroblast growth factor
C;Superfamily: fibroblast growth factor; angiogenesis; growth factor; heparin binding;
C;Keywords: alternative initiators; angiogenesis; growth factor; heparin binding;
F;1-210/Product: basic fibroblast growth factor, 18K form #status predicted <MA7>
F;65-210/Product: basic fibroblast growth factor, 18K form #status predicted
F;82-86/Region: heparin binding #status predicted
F;171-174/Region: heparin binding #status predicted
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A; Residues: 54-71 <PAN>
A; Residues: 54-71 <PAN>
R; Watson, R.; Anthony, F.; Pickett, M.; Lambden, P.; Masson, Biochem. Biophys. Res. Commun. 187, 1227-1231, 1992
A; Title: Reverse transcription with nested polymerase chain
                                                                                                                   hypothetical protein R07B7.11 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change C;Accession: T24018
R;Harris, B.
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A; Title: Purification and characterization
A; Reference number: S46253; MUID:94320639;
A; Status: preliminary; translated
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A;Map position: 4q25-4q27
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A; Residues: 39-53; 65-88 <PAT>
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LIPB_SYNY3
DXR_FUSNN
YIAL_PSESS
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HSSP; P09038; IBFF.
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P15655;
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PROSITE; PS00247; HBGF_FGF; 1.

Growth factor; Mitogen; Angiogenesis; Heparin-binding.
                                                                                             SEQUENCE
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Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
-!- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hebert J.M., Basilico C., Goldfarb M., Haub O "Isolation of cDNAs encoding four mouse FGF ficharacterization of their expression patterns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE=90201563; PubMed=2318343;
Hebert J.M., Basilico C., Goldfar
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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15-JUN-2002 (Rel. 41, Last annotation update)
Heparin-binding growth factor 2 precursor (HBGF-2) (Basic fibroblast growth factor) (BFGF) (Prostatropin).
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PD000831; HB/F_growthfact;
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HEPARIN (POTENTIAL).
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RESULT 3
FGF2_RAT
ID F_GF2
AC P131
DT 01-J
DT 01-J
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DT 15-J
DT 01-J
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DT 15-J
RAT
COC Buka
OC Mamm
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RAT F1bi
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                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                   El-Husseini A.E.-D., Paterson J.A., Myal Y., Shiu R.P.C.;
"PCR detection of the rat brain basic fibroblast growth factor (
mRNA containing a unique 3' untranslated region.";
Biochim. Blophys. Acta 1131:314-316(1992).

-i- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC
IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES
VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND
CONCENTRATION OF THESE 2 GROWTH FACTORS.

-i- SUBUNIT: MONOMER.

-i- TISSUE SPECIFICITY: FOUND IN ALL THE TISSUES EXAMINED.
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P13109;
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01-JAN-1990 (Rel. 13, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Heparin-binding growth factor 2 precursor (HBGF-2) (Basic fibroblast growth factor) (BFGF) (Prostatropin).
                                                                                 EMBL;
                                                                                                                                  or send an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Rasumarthi K.B.S., Jin Y., Cattini P.A.;
"Cloning of the rat fibroblast growth factor-2 promoter its response to mitogenic stimuli in glioma C6 cells.";
J. Neurochem. 68:898-908(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Sprague-Dawley; TISSUE-Testis. MEDLINE-97200905; PubMed-9048734;
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MEDLINE=89061721; PubMed=3196337;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kurokawa T., Seno M., Igarashi K.;
"Nucleotide sequence of rat basic fibroblast growth factor cDNA.";
Nucleic Acids Res. 16:5201-5201(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=88262516;
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                                                                                                                                                                                                            European Bioinformatics Institute. The by non-profit institutions as long
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  M22427;
X07285;
U78079;
X61697;
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                                                                                                                             and this statement is not removed requires a license agreement (See an email to license@isb-sib.ch).
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CAA30265.
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CAA43863.
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23-OCT-1986
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SEQUENCE OF 1-9.

MEDILINE-86295737; PubMed-3741423;

Ueno N., Baird A., Esch F., Ling N., Guil

"Isolation of an amino terminal extended
growth factor.";

Biochem. Biophys. Res. Commun. 138:580-58
                                                                               SEQUENCE OF 10-155.

MEDLINE-86016731; PubMed-3863109;

MEDLINE-86016731; PubMed-3863109;

Esch F., Baird A., Ling N., Ueno N., Hill F., Denoroy L., Kleppe Gospodarowicz D., Boehlen P., Guillemin R.;

"Primary structure of bovine pituitary basic fibroblast growth f (FGF) and comparison with the amino-terminal sequence of bovine
                                                                                                                                                                                                                                                                                                                                                              23-OCT-1986 (Rel. 02, Created)
23-OCT-1986 (Rel. 02, Last sequence update)
23-OCT-1986 (Rel. 02, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Heparin-binding growth factor 2 precursor (HBGF-2) (Basic fibroblast growth factor) (BFGF) (Prostatropin) [Contains: Kidney-derived growth
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ProDom; PD000831; HB/F_growt
SMART; SM00442; FGF; 1.
PROSITE; PS00247; HBGF_FGF;
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Abraham J.A., Whang J.L., Tumolo A., Mergia A., Fiddes J.C.,
Thuman basic fibroblast growth factor: nucleotide sequence,
organization, and expression in mammalian cells.";
Cold Spring Harb. Symp. Quant. Biol. 51:657-668(1986).
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-86261806; PubMed-2425435;
Abraham J.A., Mergia A., Whang J.L., Tumolo A.,
Hjerrild K.A., Gospodarowicz D., Fiddes J.C.;
"Nucleotide sequence of a bowine clone encoding
protein, basic fibroblast growth factor.";
Science 233:545-548(1986).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Bovinae; Bos.
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Growth factor;
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Pfam; PF00167; FGF; 1.
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Commun. 138:580-588(1986).
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                                                                 82:6507-6511(1985).
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MEDLINE-87119165; PubMed-3809608;

Ueno N., Baird A., Esch F., Shimasaki S., Ling N., Guillemin R.;

"Purification and partial characterization of a mitogenic factor bovine liver: structural homology with basic fibroblast growth factor.":
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-i- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND CONCENTRATION OF THESE 2 GROWTH FACTORS.

-i- SUBUNIT: MONOMER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baird A., Esch F., Boehlen P., Ling N., Gospodarowicz D.; "Isolation and partial characterization of an endothelial cell growth factor from the bovine kidney: homology with basic fibroblast growth
                                                                                                                                                                                                                                                                                                                                                               Growth factor; Mitogen;
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InterPro; IPR002348; IL1_HBGF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
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MISCELLANEOUS:
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A32878; A32878
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KIDNEY-DERIVED GROWTH FACTOR.
CELL ATTACHMENT SITE (POTENTIAL)
CELL ATTACHMENT SITE (POTENTIAL)
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RESULT 5
FGF2_HUMAN
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MEDLINE-87217066; PubMed=3472745;

MEDLINE-87217066; PubMed=3472745;

Abraham J.A., Whang J.L., Tumolo A., Mergia A., Fiddes J.C.;

Abraham J.A., Whang J.L., Tumolo A., Mergia A., Fiddes J.C.;

"Human basic fibroblast growth factor: nucleotide sequence,

"Human basic fibroblast growth factor: nucleotide sequence,

"Human basic fibroblast growth factor: nucleotide sequence,

organization, and expression in mammalian cells ";

organization, and expression in mammalian cells ";
                                                                                                                                                                                                                                                                                                                 01-NOV-1988 (Rel. 09, Last sequence of 15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Heparin-binding growth factor 2 precursor (HBGF-2) (Basic fibroblast factor) (BFGF) (Prostatropin).
growth
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                                                                                                     MEDLINE=87213238;
Sommer A., Brewer
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Gospodarowicz D., Fiddes J.
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Eukaryota; Metazoa;
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M.T., Thompson
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                                   PubMed=2435575;
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Pred. No. 0.21;
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                          Igarashi K.;
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MEDLINE=97040521; PubMed=885834;
Moy F.J., Seddon A.P., Boehlen P., P
"High-resolution solution structure
determined by multidimensional heter
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Ago H., Kitagawa Y., Fujishima ....
Ago H., Kitagawa Y., Fujishima ....
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Protein Sci. 2:1274-1284(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                          Eriksson A.E., Cousens L.S., Matthews B.W.; "Refinement of the structure of human basic at 1.6-A resolution and analysis of presumed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gautschi P., Frater-Schroeder M., Boehlen P.; 
"Partial molecular characterization of endothelial 
human brain: acidic and basic fibroblast growth fac
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MEDLINE=89184522; PubMed=2538817;
Prats H., Kaghad M., Prats A.C., Klaurun P., Chalon P., Tauber J.P.,
                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
MEDLINE=91195368; PubMed=1849658;
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MEDLINE=91195367; PubMed=1707542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Story M.T., Esch F., Shimasaki S., Sasse J., Jacobs S.C., Lawson "Amino-terminal sequence of a large form of basic fibroblast growfactor isolated from human benign prostatic hyperplastic tissue." Biochem. Biophys. Res. Commun. 142:702-709(1987).
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Gimenez-Gallego G., Conn G., Hatc
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SEQUENCE FROM
                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
                                                                                                                                                                                                                                                                                             Zhang J., Cousens L.S., Barr P.J., Sprang S.R.;
"Three-dimensional structure of human basic fibro
a structural homolog of interleukin 1 beta.";
Proc. Natl. Acad. Sci. U.S.A. 88:3446-3451(1991).
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                                                                                                                              В.Т.,
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n brain derived acidic and basic fibroblast growth factors:
terminal sequences and specific mitogenic activities.";
em. Biophys. Res. Commun. 135:541-548(1986).
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alternative CUG codons.";
Acad. Sci. U.S.A. 86:1836-1840(1989)
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              Powers R.;
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EMBL; M17599; AAA52534.1; ALT_INIT.
EMBL; X04431; CAA28027.1; -.
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EMBL; X04433; CAA28099.1; -.
EMBL; X04433; CAA28099.1; -.
EMBL; X04433; CAA28099.1; -.
EMBL; X04513; AAA52448.1; -.
EMBL; X04513; AAA52448.1; -.
EMBL; X04513; AAA52533.1; ALT_INIT.
PIR; A25824; A26642.
PIR; A26842; A26642.
PIR; B24301; B24301.
PIR; B24301; B24301.
PIR; B32878; B32878.
PIR; B32878; B32878.
PIR; S00297; S00297.
PDB; 1FC; 15-JUL-93.
PDB; 1FC; 15-JUL-93.
PDB; 1FC; 03-APR-96.
PDB; 1BFC; 03-APR-96.
PDB; 1BFC; 03-APR-96.
PDB; 1BFC; 31-JUN-97.
PDB; 1BFC; 31-JUN-96.
PDB; 1BLA; 08-NOV-96.
PDB; 1BLA; 08-NOV-96.
PDB; 1BLA; 08-NOV-96.
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Growth factor;
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PRODOMS; PD0000831; HB/F_growthfact;
SMART; SM00442; FGF; 1.
PROSITE; PS00247; HBGF_FGF; 1.
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Biochemistry 35:13552-13561(1996).
-!- FUNCTION: THE HEPARIN-BINDING
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                                                                                                                                                                                                                                                  3D-structure.
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Mitogen;
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Angiogenesis;
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CELL ATTACHMENT SITE (POTENTIAL)
HEPARIN (POTENTIAL).
HEPARIN (POTENTIAL).
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RESULT 6
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01-FEB-1996 (Rel. 3, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last annotation update)
Heparin-binding growth factor 2 precursor (HBGF-2) (Basic fibroblast growth factor) (BFGF) (Prostatropin).
FGF2 OR FGF-2.
Ovis aries (Sheep). Chordata: Craniata: Vertebrata: Buteleostomi: Bukaryota: Metazoa: Chordata: Craniata: Vertebrata: Buteleostomi:
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Submitted (SEP-1994) to
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                                                                                        modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                       Simpson R.J., Moritz R.L., Lloyd C.J., Rubira M.R., Burgess A.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pec
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           InterPro; IPR002209; HB/F_growthfact.
InterPro; IPR002348; IL1_HBGF.
Pfam; PF00167; FGF; 1.
                                                      EMBL; L36136;
PIR; S00185; S
                                                                                                                                         between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
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NCBI_TaxID=9940;
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FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC FUNCTION: THE POPTENT WITOGENS FOR A VARIETY OF CELL TYPES IN VIVO AND ARE POPTENT WITOGENS IN THE TISSUE DISTRIBUTION AND CONCENTRATION OF THESE 2 GROWTH FACTORS.
SUBUNIT: MONOMER.
SUBUNIT: MONOMER.
MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN MORE STRONGLY THAN
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PRINTS; PR00262;

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RESULT 7
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InterPro; IPR002348; IL1_HBGF.
Pfam; PF00167; FGF; 1.
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01-FEB-1996 (Rel. 33, Last sequence update)
15-JUNN-2002 (Rel. 41, Last annotation update)
Heparin-binding growth factor 2 precursor (HBGF-2) (Basic growth factor) (BFGF) (Prostatropin).
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ProDom; PD000831; HB/F_growthfact;
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HSSP; P09038; 1BFF
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Mammalia; Metatheri
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                                                                                                                                                                       European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
                                                                                                                                                                                                                                              MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN MORE STRONGLY THAN
                                                                                                                                                                                                                                                          SUBUNIT: MONOMER
                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                       PS00247; HBGF_FGF;
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Metazoa; Chordata; Craniata; Vertebrata;
etatheria; Didelphimorphia; Didelphidae;
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P75853; Q9R7Q5;
15-JUL-1998 (Rel. 3
15-DEC-1998 (Rel. 3
16-OCT-2001 (Rel. 4
                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yam Yano M., Horiuchi T.;
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                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                       use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                   "A 718-kb DNA Sequence of Escherichia coli K-12 Genome Corre to the 12.7-28.0 min Region on the Linkage Map."; but Res. 3:137-155(1996).
-i- FUNCTION: PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT ALIPHATIC SULFONATES. PUTATIVE BINDING PROTEIN.
-i- SUBCELLULAR LOCATION: Periplasmic (Potential).
-i- SIMILARITY: TO B.SUBTILIS SSUA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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STRAIN-K12 / MG16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97061202; PubMed=8905232;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complete genome sequence of Escherichia coli K-12."; nce 277:1453-1474(1997).
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     AJ237695;
AE000195;
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37, Last sequence update)
40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sulfonates
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17303 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     subdivision; Enterobacteriaceae;
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                                                                                                (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bykowski T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
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ne EMBL out
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the is in
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                                                                                                                                                                                                                                                                                                                                                                                                                         Corresponding
                                                                                                                                                                                                   a collaboration -
                                                                                                                                                                                                                                                                                                                                                  SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saito N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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BINDING
BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antisense mRNAs during chicken embryogenesis.";
Dev. Biol. 157:110-118(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions are long as its content use by non-profit institutions are long as its content use by non-profit institutions are long as its content when the long its long is the long its long in the long its l
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FGF2 OR FGF-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Heparin-binding growth factor 2 precur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMARP; SMO0062; PBPb; 1.
Transport; Periplasmic; Signal; Complete proteome.
SIGNAL 1 21 POTENTIAL.
CHAIN 22 319 PUTATIVE ALIPHATIC SU
                                                                                                                              PROPEP
                                                                                                                                                                                  SMART; SM00442; FGF; 1.
PROSITE; PS00247; HBGF_FGF;
                                                                                                                                                                                                                                                      PRINTS; PR00262; IL1HBGF, ProDom; PD000831; HB/F_gr
                                                                                                                                                                                                                                                                                                                InterPro; IPR002209; HB/F_growthfact.
InterPro; IPR002348; IL1_HBGF.
Pfam; PF00167; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M95707; AAA48617.1;
HSSP; P09038; 1BFF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-93246053; PubMed-7683281;
MEDLINE-93246053; PubMed-7683281;
Borja A.Z., Zeller R., Meijers C.;
"Expression of alternatively splic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9031;
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InterPro; IPR001638; SBP_bac_3.
SMART; SM00062; PBPb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC A IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES I VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND CONCENTRATION OF THESE 2 GROWTH FACTORS.

SUBUNIT: MONOMER.

MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN MORE STRONGLY THAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AFGE.
SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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                                Mitogen; Angiogenesis; Heparin-binding.

1 12 BY SIMILARITY.
3 158 HEPARIN-BINDING GROWTH FACTOR (POTENTIAL).
9 122 HEPARIN (POTENTIAL).
   ΑΑ;
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                                                                                                                                                                                                                                               HB/F_growthfact;
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   17374
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   HEPARIN (POTENTIAL).
HEPARIN (POTENTIAL).
7B69B684C17F1816 C
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Best Local
         SMART; SM00060; FN3; 3.

SMART; SM00410; IG_11ke; 1.

SMART; SM00408; IGC2; 1.

SMART; SM00194; PTPC; 2.

PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.

PROSITE; PS00365; TYR_PHOSPHATASE_2; 2.

PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.

PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.

Hydrolase; Receptor; Glycoprotein; Signal Cell adhesion; Immunoglobulin domain; Repp SIGNAL

23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=90046860; PubMed=2554325;
Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;
"A family of receptor-linked protein tyrosine phosphatases and Drosophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea;

Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brach

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Protein-tyrosine phosphatase DPTP
Protein-tyrosine phosphatase DPTP
                                                                                                                                                        Pfam; PF00041; fn3; 3.
Pfam; PF00047; ig; 2.
Pfam; PF00102; Y_phosphatase;
PFINTS; PR00700; PRTYPHPHTASE
                                                                                                                                                                                                                                                                                                                       EMBL; M27699; AAA288
PIR; B36182; B36182.
HSSP; P18052; 1YFO.
                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removentities requires a license agreement (Sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- SUBCELLULAR LOCATION: Type I membrane protein.
-i- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
-i- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
-i- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 86:8
-i- FUNCTION: IT IS POSSIBLE THAT
-i- CATALYTIC ACTIVITY: Protein ty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTP6_DROME
P16620;
                                                                                                                                                                                                                  InterPro; IPR003600;
InterPro; IPR000387;
InterPro; IPR000242;
                                                                                                                                                                                                                                                               InterPro; IPR003006; InterPro; IPR003598;
                                                                                                                                                                                                                                                                                                           FlyBase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      between
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                                                                                                                                                                                                                                                                                             InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tyrosine + phosphate.
SUBCELLULAR LOCATION: Type I membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WCTWDAFYLTVHPQGVIEGVRHLVD 27
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9; Conserv
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FN_III.
FIG_MHC.
FIG_C2.
FIG_1ike.
FYR_phosphatase.
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Pred. No.
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THAT DPTP IS A CELL ADHESION REVAIN TYPOSINE Phosphate + H(2)O =
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                                    PTP; 2.
Signal;
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                                          Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                             http://www.isb-sib.ch/announce/
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PROTEIN-TYROSINE

PHOSPHATASE DPTP

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Best Local
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                                                                                  MEDLINE-21595285; PubMed-11759840; MEDLINE-21595285; PubMed-11759840; MEDLINE-21595285; PubMed-11759840; Kuritz T., Sasamoto S., Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Kaneko T., Nakamura Y., Kimura M., Tshikawa A., Kawashima K., Kimura Matsuno A., Muraki A., Matsuno A., Muraki A., Matsuno A., Muraki A., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M.,
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ACT_SITE
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TRANSMEM
     cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
-i- CATALYTIC ACTIVITY: L-histidinol-phosphate + 2-oxogl
(imidazol-4-yl)-2-oxopropyl phosphate + L-glutamate.
-i- COFACTOR: Pyridoxal phosphate (By similarity).
-i- PATHWAY: Histidine biosynthesis; seventh step.
                                                                       Kishiru
Nakazaki N., Shing
Nakazaki N., Tabata
                                                                                                                                                                                                      HI81_ANASP STANDARD; PRT; 353 AA. 08YV89; 05YV89; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Histidinol-phosphate aminotransferase 1 (EC 2
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DOMAIN
                                                     "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
                                                                                 Kishida Y., Kohara M., Matsumoto
Nakazaki N., Shimpo S., Sugimoto
                                                                                                                                                       Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales;
MCBI_TaxID=103690;
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FIBRONECTIN TYPE-III 2.
PROTEIN-TYROSINE PHOSPHATASE 1
PROTEIN-TYROSINE PHOSPHATASE 2
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                              Score 52; DB Pred. No. 24; 6; Mismatches
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CYTOPLASMIC (POTENTIAL).
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IG-LIKE C2-TYPE DOMAIN 2.
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                                    2-oxoglutarate =
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Best Local :
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P11319;
01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 21, Last sequence update 01-AUG-1992 (Rel. 23, Last annotation update probable early E3 12.1 kDa glycoprotein.
Human adenovirus type 3.
Viruses; dsDNA viruses, no RNA stage; Ader NCBL_TaxID-45659;
                                                                                                                                                                            PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signaes C., Akusjaervi G., Pettersson U.; "Region E3 of human adenoviruses; differences between the oncogenic adenovirus-3 and the non-oncogenic adenovirus-2."; Gene 50:173-184(1986).
                                                                                                                               Early protein; Glycoprotein. CARBOHYD 77 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADE03
                                                                                                       SEQUENCE
                                                                                                                                                                                                         EMBL; M15952;
                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - between Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Histidine biosynthesis; Transferase; Aminotransferase; Pyridoxal phosphate; Complete proteome.
BINDING 211 211 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AP003588; BAB73791.1; Interpro; IPR004839; Aminotransf1/2. Interpro; IPR001917; Wittransf 2. Pfam; PF00155; aminotran_1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: NOT YET KNOWN.
-!- SIMILARITY: TO EQUIVALENT PROTEIN IN OTHER ADENOVIRUSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=87219876; PubMed=3582978;
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PROSITE; PS00599; AA_TRANSFER_CLASS_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (for send an email to license@isb-sib.ch)
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Best Local
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PIP_NEIGO
P4786;
01-NOV-1995 (
01-NOV-1995 (
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  Escherichia
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YAED OR B0200
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ACT_SITE
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InterPro; IPR002410; Pro_amnoPTase.
InterPro; IPR002379; Ser_estrs_site.
Pfam; PF00561; abhydrolase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Albertson N.H., Koomey M.; "Molecular cloning and characterization of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95020651; PubMed=7934933;
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SEQUENCE FROM N.A., ANI
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Bacteria; Proteobacteria;
NCBI_TaxID=485;
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               -JUL-1993 (Rel. 26, Created)
-JUL-1993 (Rel. 26, Last seque-
-CT-2001 (Rel. 40, Last anno-
pothetical protein yaeD.
ED OR B0200 OR Z0212 OR ECS02
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FUNCTION: HYDROLYSES PEPTIDES HAVING THE VIELD FREE PROLINE. ALSO HYDROLYSES THE CATALYTIC ACTIVITY: Release of a N-termin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO PEPTIDASE FAMILY S33.
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9; Conserv
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Pred. No. 12;
7; Mismatches
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PROTON DONOR (BY SIMILARITY).
DOE7AEBA908A1AEO CRC64;
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STRAIN-0157:H7 / RIMD 0509952;

MEDLINE-2115C31; PubMed-11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001).

-I- SIMILARITY: TO M.JANNASCHII MJ0015.

-I- SIMILARITY: TO M.JANNASCHII MJ0015.

-I- SIMILARITY: TO M.JANNASCHII MJ0015.
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Blattner F.R., Plunkett G. III, Bloch C.,
Riley M., Collado-Vides J., Glasner J.D.,
Gregor J., Davis N.W., Kirkpatrick H.A.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                   Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K. Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R., Welch R.A., Blattner F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Takemoto K., Mori H., Murayama N., Kataoka K., Yano M., Itoh T. Yamamoto Y., Inokuchi H., Miki T., Hatada E., Fukuda R., Ichiha Mizuno T., Makino K., Nakata A., Yura T., Sampei G., Mizobuchi "Systematic sequencing of the Escherichia coli genome: analysis 4.0 - 6.0 min (189,987 - 281,415bp) region."; Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
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  This SWISS-PROT entry is copyright. It is produced through
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MEDLINE=21074935; PubMed=11206551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Rurokawa K., Yasunaga T., Makino K., Shinagawa H
"Development of primer sets for direct sequence
the ribosomal operons of Escherichia coll.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ da
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-0157:H7 / RIMD 0509952;
Ohnishi M., Murata T., Nakayam
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A., Goeden M.A., Rose D.J.,
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P74519;
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MEDLINE-97061201; pubMed-8905231;
MEDLINE-97061201; pubMed-8905231;
MEDLINE-97061201; pubMed-8905231;
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InterPro; IPRO04446; Hstdl_phs_rel.
Pfam; PF00702; Hydrolase; 1.
TIGRFAMs; TIGR00213; hstdl_phs_rel; 1.
Hypothetical protein; Complete proteom
SEQUENCE 191 AA; 21294 MW; E7814B3
                                              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                  EMBL;
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lipoate-protein ligase B (EC 6.-.-) (Lipoate biosynthesis protein
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EMBL; AE005159; AAG54502.1; -.
EMBL; AP002550; BAB33625.1; -.
ECOGene; EG11736; yaeD.
InterPro;
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                                                                                                                                                                                                            RESIDUE IN LIPOYLATED PROTEINS (BY SIMILARITY).
PATHWAY: Lipoate biosynthesis.
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                            SIMILARITY: BELONGS TO THE LIPB FAMILY.
                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                  D90915;
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Pfam; PF03099; BPL_LipA_LipB; 1
ProDom; PD006086; Lipoate_B; 1.
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Q942T6;
Q942T6;
01-DEC-2001
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09ZT62; PREMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohsumi C., Nozaki J., Kida T.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF073744; AAAD02832.1; -
Glycosyltransferase; Transferase.
SEQUENCE 784 AA; 86920 MW; 3B06A491F0908933 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cucumis sativus (Cucumber).

Cucumis sativus (Cucumber).

Cukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Roside eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE-LEAF;
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l (TrEMBLrel. 19,
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                                                                                                                                             PRELIMINARY;
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Q9FND9;
Q9FND9;
Q9FND9;
T01-MAR-2001 (TrEMBLrel. 16, Created)
T01-MAR-2001 (TrEMBLrel. 21, Last sequence update)
T01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Raffinose synthase protein.
N MP012:13.
Arabidopsis thaliana (Mouse-ear cress).
Spermatophyta; Wagnoliophyta; eudicotyledons; core eud
Eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Q8VWN6;
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JAN-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pisum sativum (Garden pea).
Eukaryota; Viridiplantae; Stre
Eukaryota; Magnoliophyta;
Spermatophyta; Magnoliophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1 clone:P0583CO8.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases EMBL; AP003382; BAB64768.1;
SEQUENCE 816 AA; 89588 MW; B316EDF3566C5178 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transferase; Glycosyltransferase. SEQUENCE 798 AA; 88717 MW; 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-CV. WUNDER VON KELVEDON; TISSUE-SEED;
Peterbauer T. Mach L., Mucha J., Richter A.;
"Molecular characterization of raffinose synt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eurosids
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01-MAR-2002 (TrembLrel.
01-MAR-2002 (TrembLrel.
Raffinose synthase (EC 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-CV.
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NCBI_TaxID-4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3888;
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l Similarity 83.3%;
25; Conservative
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20, Last sequence update;
20, Last annotation updat;
2.4.1.82).
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of raffinose synthase
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1; Mismatches
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Pred. No. 4.
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Pred. No. 6
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.2e-13;
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                              core eudicots;
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H. Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozak. Ecker J., Theologis A., Davis R.W.;
Submitted (NOV-2001) to the Ever T.
                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core en Asteridae; euasterids I; Lamiales; Lamiaceae; Stachys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carnincí P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J., Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Scker J., Theologis A., Davis R.W.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AB006702; BAB11595.1; -. EMBL; AY081645; AAM10207.1; -. EMBL; AY081645; AAM10207.1; -.
                                                     EMBL; AJ344091; CAC86963.1; --
Transferase; Glycosyltransferase
SEQUENCE 863 AA; 95227 MW; DI
                                                                                          "Molecular cloning of a cDN/
Stachys sieboldii.";
Submitted (AUG-2001) to the
                                                                                                                                              TISSUE=LEAF;
                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                      Stachys affinis
                                                                                                                                                                                                                                                                                                                            Q8RW08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Structural analysis of Arabidopsis Sequence features of the regions of physically assigned Pl clones.";
                                                                                                                                 Pesch M., Schmitz K.;
                                                                                                                                                                                  NCBI_TaxID=168825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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MEDLINE=98069011; PubMed=9405937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=3702;
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4:291-300(1997).
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69.0%;
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                                                                                          EMBL/GenBank/DDBJ
  Score 124; DE Pred. No. 7.8e 2; Mismatches
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7.8e-09;
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Matches 19
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Best Local
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  093XK2
093XK2;
01-DEC-2001
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Q43408;
01-NOV-1996
01-NOV-1996
01-DEC-2001
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BMBL; Y19024; CAB64363.1; -...
Clycosyltransferase. Transferase.
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01-MAY 2000 (TrEMBLrel. 20, Last sequence update)
01-MAR 2002 (TrEMBLrel. 20, Last annotation update)
01-MAR 2002 (TrEMBLrel. 20, Last annotation update)
Galactinol-raffinose galactosyltransferase (EC 2.4.1.67).
Phaseolus angularis (Adzuki bean) (Vigna angularis; Tracheophyta; Eubryophyta; Tracheophyta; Eubryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Putative imbibition protein.

Brassica oleracea (Cauliflower).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-CV. ALPHA BALOMA; TISSUE-ROOT TIPS;
STRAIN-CV. ALPHA BALOMA; TISSUE-ROOT TIPS;
FUJIKUTA Y., Karssen C.K.;
FUJIKUTA Y., Karssen C.K.;
"Cauliflower cDNA encoding a putative imbibition protein.";
Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
SEMBL; X79330; CAAS5893.1; -.
SEQUENCE 765 AA; 84084 MW; 73398603048E9B58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3712;
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19; Conser
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
      (TrEMBLrel.
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94949 MW; 85248C4B81165679
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Pred. No. 4.56
3; Mismatches
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Pred. No. 7.4e-08;
4; Mismatches 6
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Spermatophyta;
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RESULT 10
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Best Local S
Matches 18
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Best Local 9
                                                                                                                            Q40077
Q40077;
Q1-NOV-1996
Q1-NOV-1996
Q1-DEC-2001
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Q39466;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation updat
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Pisum sativum (Garden pea).

Pisum sativum (Garden pea).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
                                                                                SIP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids I; Fabales; Fabaceae; Papillonoideae; Cicereae; Cicer. NCBI_TaxID=3827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAY 2001) to the ELEMBL; AJ311087; CAC38094.1; -Glycosyltransferase; TransferseQUENCE 853 AA; 95890 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Stachyose synthase (EC 2.4.1.67).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular cloning seeds.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CV. WUNDER VON KELVEDON; Peterbauer T.;
                            Hordeum vulgare (Barley).
Eukaryota; Viridiplantae;
                                                                                                     Seed imbibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
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18; Conser
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357 AA;
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6 (TrEMBLrel.
1 (TrEMBLrel.
                                                                                                                                                                                                                                  PRELIMINARY;
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     Magnoliophyta;
                                                                                                     protein.
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62.1%;
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01,
19,
Streptophyta; En
yta; Liliopsida;
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Last sequence up
Last annotation
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Pred. No. 5
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Pred. No. 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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  Embryophyta; Tracheophyta;
a; Poales; Poaceae; Pooldea
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     Pooideae;
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                                                                                     Q94A08 PRELIMINARY; PRT; 773 AA.

C Q94A08;
C Q94A08;
T 01-DEC-2001 (TrEMBLrel. 19, Created)
T 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
T 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
T 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
E Putative imbibition protein.
S Arabidopsis thaliana (Mouse-ear cress).
E Putatyota; Viridiplantae; Streptophyta; Embryophyta: Trac
C Eukaryota; Viridiplantae; Streptophyta; Core eudic
C Eukaryota; Viridiplantae; Brassicaceae; Arabidopsis.
C Eukaryota; Magnoliophyta; eudicotyledons; core eudic
C eurosids I; Brassicales; Brassicaceae; Arabidopsis.
X NCBL_TaxID-3702;
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Q9SCM1;

Q9SCM1;

Q1-MAY-2000 (TrEMBLrel. 13, Cr

Q1-MAY-2000 (TrEMBLrel. 13, Lr

Q1-MAY-2000 (TrEMBLrel. 13, Lr

Q1-MAY-2000 (TrEMBLrel. 13, Lr
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eu

Burassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
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Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases
EMBL; M77475; AAA32975.1;
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    SEQUENCE FROM N.A. Yamada K., Liu S.X., Goldsmith A.D., Jian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EU Arabidopsis sequencing project;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ
EMBL; AL133248; CAB66109.1; -
SEQUENCE 773 AA; 85143 MW; 0852F9E67952C8E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Benes V., Rechmann S., Borko
Bayer K.F.X., Quetier F., Sa
Submitted (NOV-1999) to the
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loning and characterization
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J.M., Onodera (
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1.2e-06;
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  Dale J., Quach
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Q9M4M7
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Q9M4M7 Q9M4M7; 01-OCT-2000 01-OCT-2000

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C Q9SYJ4;
C Q9SYJ4;
T 01-MAY-2000 (TrEMBLrel. 13, Created)
T 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
T 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
P Putative raffinose synthase OR seed IMBIBITION protein.
N T7B11.23 OR AM4G01970.
S Arabidopsis thaliana (Mouse-ear cress).
C Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trac
Spermatophyta; Magnoliophyta; eudicotyledons; core eudic
c eurosids II; Brassicales; Brassicaceae; Arabidopsis.
N NCBL_TaxID=3702;
                                                                                                                                                                                                         SEQUENCE FROM N.A.
Spiegel L.A., Huang E.N., Nascimento
Spiegel L.A., Huang E.N., Shah R., O'Shaughnessy
Preston R.R., Matero A., Shah R., O'Shaughnessy
Shekher M., Schutz K., See L.H., Swaby I., Habo
Shekher M., Lemoke K., Mayer K.F.X.;
Mewes H.W., Lemoke K., Mayer K.F.X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayshizzaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R. W., Ecker J.R., Theologis A.; "Full Length cDNA of gene T8H10.120/AT3g57520 (GI:6706423)."; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AV050772; AAX92707.1; "SEQUENCE 773 AA; 85171 MW; 18BDF9E67952C801 CRC64;
                                                                                                                                                                                                                                                                                                                                      Huang E.N., Nascimento L., de la Bastide M., Hab
Preston R.R., Spiegel L.A., See L.H., Shah R., w
O'Shaughnessy A., Rodriguez M., Shekher M., Swat
Parnell L.D., Dedhia N.N., McCombie W.R.;
"Arabidopsis thaliana BAC T7B11 from chromosome
Submitted (APR-1999) to the EMBL/GenBank/DDBJ da
                                                                                                                      EU Arabidopsis sequencing pr
Submitted (MAR-2000) to the
EMBL; AC007138; AAD22659.1;
EMBL; AL161493; CAB80690.1;
SEQUENCE 807 AA; 90122 MW
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235
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FGWCTWDACYLTVDPATIWTGVKEFEDGG
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18; Conser
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Lrel. 15, Last annotation update)
Synthase OR seed IMBIBITION protein.
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62.1%;
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Shah R., O'Shaughnessy &
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                                                      Pred. No. 2.46
2; Mismatches
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Pred. No. 1.
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Swaby I.,
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Schutz
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Q8RX87;
O1-JUN-2002 (TrEMBLrel. 21, Created)
O1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
AT5920250/F5024_140.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

STRAIN-CV. HASS; TISSUE-MESOCARP;

Zamorano J.P., Evans A.D., Dopico B., Lowe A.L., Wilson I.D.,

Merodio C., Grierson D.;

"Isolation and characterization of cDNAs for mRNAs regulated during
cold storage of avocado (Persea americana Mill.) fruit.";

Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ133148; CAB77245.1;

EMBL; AJ133148; CAB77245.1;

SEQUENCE 779 AA; 85368 MW; C3A8B43160316785 CRC64;
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 SIP.
                                                                                                                                                                                                                                                                        Shinn P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J., Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G. Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Persea americana (Avocado).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Persea.
NCBI_TaxID=3435;
                                                                                                                                                                                            "Arabidopsis cDNA clones.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY090237; AAL90901.1; -.
SEQUENCE 844 AA; 94215 MW; 2AC8AB0EA43F8056 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FGWCTWDAFYLTVHPQGVIEGVRHLVDGG
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                                                                               FGWCTWDAFYLTVHPQGVIEGVRHLVDGG 29
                                                              FGWCTWDAFYQEVTQEGVEAGLKSLAAGG
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17; Conservative
               27,
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               2003, 10:05:56
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; Pred. No. 1.2e
4; Mismatches
                                                                                                                             Score 99; DB 10;
Pred. No. 2.4e-05;
3; Mismatches 9
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Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/Pications_AD:*

2: /cgn2_6/ptodata/2/pubpaa/Pications_AD:*

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10: /cgn2_6/ptodata/2/Uications_AD:*

10: /cgn2_6/ptodata/2/pubpaa/Uications_AD:*

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1 FGWCTWDAFYI.TVH
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                                                                                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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253.439 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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US-10-131-065-3 US-10-131-965-5 US-10-108-195-2 US-10-108-195-3 US-10-108-195-4 US-10-108-195-7 US-09-802-365-2 US-09-8771-302-2 US-09-8771-302-2 US-09-866-856-2 US-09-866-856-8 US-10-016-447-8 US-10-016-447-8 US-10-018-195-1 US-09-822-485-5 US-09-822-485-5	US-09-901-938-24	ID
Sequence 3, Appli Sequence 5, Appli Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 7, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 5, Appli	24,	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21
48	48	48	48	48	48	48.5	48.5		48.5	49	51.5	52	53.5	60	60	60	60	60	60	60	60	60	60	60
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207	207	207	207	207	141	592	497	497	161	140	280	313	333	501	333	210	159	158	155	155	155	155	155	155
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US-09-817-814-24	US-09-805-805-7	US-09-805-805-5	US-09-750-963-6	US-09-822-485-19	US-09-901-938-18	US-09-753-126-4	US-09-753-126-1	US-09-896-896A-1	US-09-893-737-288	JS-10-131-965-2	US-09-815-242-11714	US-09-788-626-19	US-09-815-242-10116	US-09-934-706-4	US-10-108-195-6	US-09-902-773A-4	US-09-934-706-2	US-09-826-210-2	US-09-749-728B-7	US-09-886-856-8	US-09-886-856-6	US-09-425-021-10	US-09-251-263-10	US-09-802-365-8
24,	Sequence 7, Appli		Sequence 6, Appli	Sequence 19, Appl	Sequence 18, Appl	Sequence 4, Appli	Sequence 1, Appl1	Sequence 1, Appli	Sequence 288, App	Sequence 2, Appli	Sequence 11714, A	Sequence 19, Appl	Sequence 10116, A	Sequence 4, Appli	Sequence 6, Appli	Sequence 4, Appli	'n	Sequence 2, Appli	Sequence 7, Appli	Sequence 8, Appli	Sequence 6, Appl1	Sequence 10, Appl	Sequence 10, Appl	Sequence 8, Appli

ALIGNMENTS

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RESULT 2
US-09-940-601-3
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; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-901-938-24
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; Sequence 24, Application US/09901938
; Patent No. US20020156001A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: ECONS, MICHAel
APPLICANT: ECONS, MICHAel
APPLICANT: WHITE, Kenneth
APPLICANT: STROM, Tim
APPLICANT: MEITINGER, Thomas
APPLICANT: MEITINGER, Thomas
TITLE OF INVENTION: NOVEL FIBROBLAST GROWTH FACTOR (FGF23) AND METHODS FOR USE
FILE REFERENCE: 053884-5001
                                                                                                  GENERAL INFORMATION:
                                                                                                                     Sequence 3, Application US/09940601
Publication No. US20030004319A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.0 SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                            Query Match 33.1%;
Best Local Similarity 40.0%;
Matches 10; Conservative
APPLICANT: Basilico, Claudio
APPLICANT: Delli Bovi, Pasquale
TITLE OF INVENTION: MAMMALIAN GROWTH FACTOR
FILE REFERENCE: 5986/13586-0SC
CURRENT APPLICATION NUMBER: US/09/940,601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/219,137
PRIOR FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 34
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PRIOR APPLICATION NUMBER: 08/056,482 PRIOR FILING DATE: 1993-05-03

PRIOR APPLICATION NUMBER: 08, PRIOR FILING DATE: 1996-12-31

2001-08-27 BER: 08/775,567

CURRENT FILING DATE:

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; TYPE: PRT; ORGANISM: Human FGF-2US-10-131-965-3
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Best Local Similarity
Watches 10; Conserve
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                                                                                                                                  Sequence 5, Application US/10131965
Patent No. US20020165160A1
GENERAL INFORMATION:
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APPLICANT: Whitehouse, Martha J.
APPLICANT: Kavanaugh, Michael W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 3
APPLICANT: Whitehouse, Martha J.
APPLICANT: Kavanaugh, Michael W.
TITLE OF INVENTION: Angiogenically Effective Unit Dose of FGF and Method of
TITLE OF INVENTION: Administering
FILE REFERENCE: 1296/12169US05
CURRENT APPLICATION NUMBER: US/10/131,965
CURRENT FILING DATE: 2002-04-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Angiogenically Effective Unit Dose of FGF and Method TITLE OF INVENTION: Administering FILE REFERENCE: 1296/12169US05 CURRENT APPLICATION NUMBER: US/10/131,965 CURRENT FILING DATE: 2002-04-25
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PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 15
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PRIOR TILING DATE: 1991-12-06
PRIOR APPLICATION NUMBER: 07/177,506
PRIOR FILING DATE: 1988-04-04
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ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 146
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US-10-108-195-3
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                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Kwan, Chi
APPLICANT: Venkatar
APPLICANT: Shriver,
APPLICANT: Raman, R
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                                                                                                                                                                                                                                Sequence 3, Application US/10108195 Publication No. US20030008820A1
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LENGTH: 146
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APPLICANT:
APPLICANT:
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Matches 10; Conservative
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Publication No.
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FILE REFERENCE: M00656/70076
CURRENT APPLICATION NUMBER: US/10/108,195
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 60/279,165
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 15
                                                                                                         APPLICANT: Sasisekharan, Ram TITLE OF INVENTION: Methods and Products Related to FGF Dimerization
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PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 15
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CURRENT FILING DATE: 2002-03-27
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APPLICANT: Venkataraman, Ganesh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Mutant of Native FGF2 with 9 N-terminal Residues Deleted
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                                                                                                                                                          Shriver,
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Pred. No. 0.
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APPLICANT: Raman, Rahul
APPLICANT: Sasisekharan, Ram
TITLE OF INVENTION: Methods and Products Related to
FILE REFERENCE: M00656/70076
CURRENT APPLICATION NUMBER: US/10/108,195
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 60/279,165
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
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US-10-108-195-4
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Best Local Similarity 40...
10; Conservative
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Publication No. US20030008820A1
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Best Local Similarity
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APPLICANT: Raman, Rahul
APPLICANT: Sasisekharan, Ram
TITLE OF INVENTION: Wethods and Products Related
FILE REFERENCE: M00656/70076
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APPLICANT: Venkataraman, Ganesh
APPLICANT: Shriver, Zachary
CURRENT APPLICATION NUMBER: US/10/108,195
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 60/279,165
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                APPLICANT: Kwan, Chi-Pong APPLICANT: Venkataraman,
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TYPE: PRT
ORGANISM: Artificial Sequence
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Pred. No. 0.55;
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APPLICANT: Whitehouse, Martha Jo
TITLE OF INVENTION: Methods and Compositions for the
TITLE OF INVENTION: Treatment and Prevention of Erectile Dys
FILE REFERENCE: 1671.003
CURRENT APPLICATION NUMBER: US/09/802,365
CURRENT FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/188,480
PRIOR FILING DATE: 2000-03-10
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 60/203,415
PRIOR FILING DATE: 2000-05-11
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
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GENERAL INFORMATION:
APPLICANT: Whitehouse, Martha Jo
TITLE OF INVENTION: Methods and Compositions for the
TITLE OF INVENTION: Treatment and Prevention of Erectile Dysfunction
FILE REFERENCE: 1671.003
FILE REFERENCE: 1671.003
CURRENT APPLICATION NUMBER: US/09/802,365
CURRENT EILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/188,480
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Best Local Similarity 40.0
Matches 10; Conservative
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                                                                                                                                                    SEQ ID NO 4
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                   Query Match
Best Local
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Best Local
     Matches
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PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-05-11
                                                                                                                                                                    NUMBER OF SEQ ID NOS: 9 SOFTWARE: FastSEQ for Windows Version
                                                                                           ORGANISM: Homo sapiens
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                                                                                                                TYPE: PRT
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Score 60; DB 10;
Pred. No. 0.55;
5; Mismatches 10
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WCTWDAFYLTVHPQGVIEGVRHLVD

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RESULT 13
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TYPE: PRT
ORGANISM: Bos taurus
US-09-886-856-2
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Best Local Similarity
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Patent No. US20020072489A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Whitehouse, Martha Jo
TITLE OF INVENTION: Methods and Compositions
TITLE OF INVENTION: Treatment of Peripheral
FILE REFERENCE: PP16090.004
CURRENT APPLICATION NUMBER: US/09/886,856
CURRENT FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: 60/213,504
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TITLE OF INVENTION: Anglogenically Effective Unit Dose of FGF-2 and Method
TITLE OF INVENTION: Of Use
FILE REFERENCE: 1296/12169US04
CURRENT APPLICATION NUMBER: US/09/771,302
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/385,114
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/276,549
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 9
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PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/264,572 PRIOR FILING DATE: 2000-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 146
                                                         24 YCKNGGFFLRIHPDGRVDGVREKSD 48
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                                                                                           3 WCTWDAFYLTVHPQGVIEGVRHLVD 27
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                                                                                                                                    Conservative
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                                                                                                                                                    33.1%;
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; Pred. No. 0.55
5; Mismatches
                                                                                                                                                      Score 60; I
                                                                                                                                    Mismatches
                                                                                                                                                    DB 10;
0.55;
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0.55;
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                                                                                                                                  10;
                                                                                                                                                                         Length 146;
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                                                                                                                                  0;
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US-09-820-596-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Fast
SEQ ID NO 4
LENGTH: 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/09820596 Publication No. US20030022170A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/213,504
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/264,572
PRIOR FILING DATE: 2000-01-26
PRIOR APPLICATION NUMBER: 60/276,549
PRIOR FILING DATE: 000-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Whitehouse, Martha Jo
TITLE OF INVENTION: Methods and Compositions for the
TITLE OF INVENTION: Treatment of Peripheral Artery (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/886,856
CURRENT FILING DATE: 2001-06-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: PP16090.004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                       INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 YCKNGGFFLRIHPDGRVDGVREKSD 48
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mes 10; Conserv
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                APPLICATION NUMBER: 09/036,594
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Arnold E., Beth
                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/820,596 FILING DATE: 29-Mar-2001 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL INFORMATION:
AL INFORMATION:
APPLICANT: Khodadoust, Mehran Mohammad
APPLICANT: Khodadoust, Mehran Mohammad
TITLE OF INVENTION: NOVEL FIBROBLAST GROWTH FACTORS AND
THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
                                                                                                                                                                              REFERENCE/DOCKET NUMBER: MIA-026.01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FastSEQ for Windows Version 4.0
TOPOLOGY: line
                                            TYPE: amino acid
                                                                                                                                                       TELEPHONE: 617-832-1000
                                                                                                                                                                                                                           REGISTRATION NUMBER: 35,430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
STATE: MA
                                                               LENGTH: 147 amino acids
                                                                                                                                    TELEFAX: 617-832-7000
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Pred. No. 0.
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Sequence 8, Application US/10016447

Patent No. US20020090651A1

GENERAL INFORMATION:

APPLICANT: Kirschner, Marc W.

APPLICANT: WISS-01A2

CURRENT APPLICATION NUMBER: US/10/016,447

CURRENT FILING DATE: EARLIER APPLICATION NUMBER: US/08/776,207

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/441,629

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/441,629

PRIOR FILING DATE: EARLIER FILING DATE: 1995-05-15

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/279,217

PRIOR FILING DATE: EARLIER FILING DATE: 1994-07-22

NUMBER OF SEQ ID NOS: 18

SOPTWARE: FastSEQ for Windows Version 3.0

LENGTH: 150

TYPE: PRT

ORGANISM: Homo sapien
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US-10-016-447-8
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Search completed: March 27, 2003, 10:20:35 Job time: 6.95122 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 33.1%; Score 60; DB 9; Length 147; Best Local Similarity 40.0%; Pred. No. 0.55; Matches 10; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                Query Match 33.1%;
Best Local Similarity 40.0%;
Matches 10; Conservative
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:| |:| :|| |:||| |
25 YCKNGGFFLRIHPDGRVDGVREKSD 49
                                                                                                         33 YCKNGGFFLRIHPDGRVDGVREKSD 57
                                                                                                                                     3 WCTWDAFYLTVHPQGVIEGVRHLVD 27
                                                                                                                                                                                                                Score 60; DB 12; Length 150;
Pred. No. 0.56;
5; Mismatches 10; Indels
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